

Genetic Diversity and Distribution of *Peromyscus*-Borne Hantaviruses in North America

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The 1993 outbreak of hantavirus pulmonary syndrome (HPS) in the southwestern United States was associated with Sin Nombre virus, a rodent-borne hantavirus; The virus' primary reservoir is the deer mouse (*Peromyscus maniculatus*). Hantavirus-infected rodents were identified in various regions of North America. An extensive nucleotide sequence database of an 139 bp fragment amplified from virus M genomic segments was generated. Phylogenetic analysis confirmed that SNV-like hantaviruses are widely distributed in *Peromyscus* species rodents throughout North America. Classic SNV is the major cause of HPS in North America, but other Peromyscine-borne hantaviruses, e.g., New York and Monongahela viruses, are also associated with HPS cases. Although genetically diverse, SNV-like viruses have slowly coevolved with their rodent hosts. We show that the genetic relationships of hantaviruses in the Americas are complex, most likely as a result of the rapid radiation and speciation of New World sigmodontine rodents and occasional virus-host switching events.

Hantaviruses, rodent-borne RNA viruses, can be found worldwide. The Old World hantaviruses, such as Hantaan, Seoul, and Puumala, long known to be associated with human disease, cause hemorrhagic fever with renal syndrome of varying degrees of severity (1). After hantavirus pulmonary syndrome (HPS) was discovered in the southwestern United States in 1993 (2-4), intensive efforts were begun to detect and characterize hantaviruses in North America and determine their public health importance (5). As of January 1999, 205 HPS cases had been confirmed in 30 states of the United States, and 30 cases had been confirmed in three provinces of Canada; most cases occurred in the western regions of both countries. While Sin Nombre virus (SNV) has been identified as the cause of most HPS cases in

North America, an increasingly complex array of additional hantaviruses has appeared (Table 1).

Surveys of rodents for hantavirus antibody have shown hantavirus-infected rodents in most areas of North America (3;6-9; Ksiazek et al., unpub. data; Artsob et al., unpub data). Serologic evidence of hantavirus infection has been found in North American rodents of the family *Muridae*. Most North American hantaviruses are associated with the subfamily *Sigmodontinae*; only a small number are associated with the subfamilies *Arvicolinae* or *Murinae*. To determine the number and distribution of hantaviruses in North America, we conducted a nucleotide sequence analysis of a polymerase chain reaction (PCR) fragment amplified from a large number of representative HPS patient and hantavirus-infected rodent samples from throughout the region. We focused on the North American viruses (particularly those associated with *Peromyscus* species rodents), although the nucleotide sequences of many hantaviruses from

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Table 1. Hantaviruses in the New World

Virus ^a	Disease ^b	Known or suspected host	Location	Virus isolate
<i>Sigmodontinae</i> associated				
Sin Nombre	HPS	<i>Peromyscus maniculatus</i> (grassland form)	West & Central U.S. and Canada	Y
Monongahela	HPS	<i>P. maniculatus</i> (forest form)	Eastern U.S. and Canada	N
New York	HPS	<i>P. leucopus</i> (eastern haplotype)	Eastern U.S.	Y
Blue River		<i>P. leucopus</i> (SW/NW haplotypes)	Central U.S.	N
Bayou	HPS	<i>Oryzomys palustris</i>	Southwestern U.S.	Y
Black Creek Canal	HPS	<i>Sigmodon hispidus</i> (eastern form)	Florida	Y
Muleshoe		<i>S. hispidus</i> (western form)	Southern U.S.	N
Caño Delgadito		<i>S. alstoni</i>	Venezuela	Y
Andes	HPS	<i>Oligoryzomys longicaudatus</i>	Argentina and Chile	Y
Oran	HPS	<i>O. longicaudatus</i>	Northwestern Argentina	N
Lechiguanas	HPS	<i>O. flavescens</i>	Central Argentina	N
Bermejo		<i>O. chacoensis</i>	Northwestern Argentina	N
Hu39694	HPS	Unknown	Central Argentina	N
Pergamino		<i>Akodon azarae</i>	Central Argentina	N
Maciel		<i>Bolomys obscurus</i>	Central Argentina	N
Laguna Negra	HPS	<i>Calomys laucha</i>	Paraguay and Bolivia	Y
Juquitiba	HPS	Unknown	Brazil	N
Rio Mamore		<i>O. microtis</i>	Bolivia and Peru	Y
El Moro Canyon		<i>Reithrodontomys megalotis</i>	Western U.S. and Mexico	N
Rio Segundo		<i>R. mexicanus</i>	Costa Rica	N
<i>Arvicolinae</i> associated				
Prospect Hill		<i>Microtus pennsylvanicus</i>	N. America	Y
Bloodland Lake		<i>M. ochrogaster</i>	N. America	N
Prospect Hill-like		<i>M. pennsyl./montanus/ochrogaster</i>	N. America	N
Isla Vista		<i>M. californicus</i>	Western U.S. and Mexico	N
<i>Murinae</i> associated				
Seoul	HFRS	<i>Rattus norvegicus</i>	Worldwide	Y

^aMajor virus types or species are in bold and indented below the rodent subfamilies with which they are associated; related genetically distinct virus lineages that may represent additional species or subspecies are indented below virus types and species.

^bHPS = hantavirus pulmonary syndrome; HFRS = hemorrhagic fever with renal syndrome.

South America and elsewhere were included as outgroups to increase the resolution of the analysis.

Genetic Detection and Phylogenetic Analysis of New World Hantaviruses

The nucleotide sequences of 139 bp fragments of the G2 encoding region of virus M segments amplified by reverse transcriptase-PCR (RT-PCR) from 288 hantavirus-infected rodent and human samples were compiled from Genbank sources or from data reported here. Details of the specimen selection and methods of genomic analysis are provided in the Appendix. The Genbank accession numbers of those sequences published earlier (bigtree.xls) can be accessed from this article published on the journal home page (<http://www.cdc.gov/eid>). The

entire aligned dataset (bigtree.nex), including 130 newly presented sample sequences, is also available on line. These sequences include those derived from 229 SNV-like viruses associated with *Peromyscus* species rodents from throughout North America. Maximum parsimony analysis of the aligned sequences was conducted with PAUP (12; Appendix), which resulted in a reasonably well-defined tree topology with several distinct lineages of SNV-like viruses and other clearly discernable hantaviruses (Figures 1, 2). Bootstrap analysis showed that while several of the major nodes of the tree were not well supported (values of 50% or less), many others were robust (values of 70% or higher) (Figures 1, 2). In most phylogenetic analyses, bootstrap values provide highly conservative estimates of the probability of correctly inferring

Figure 1

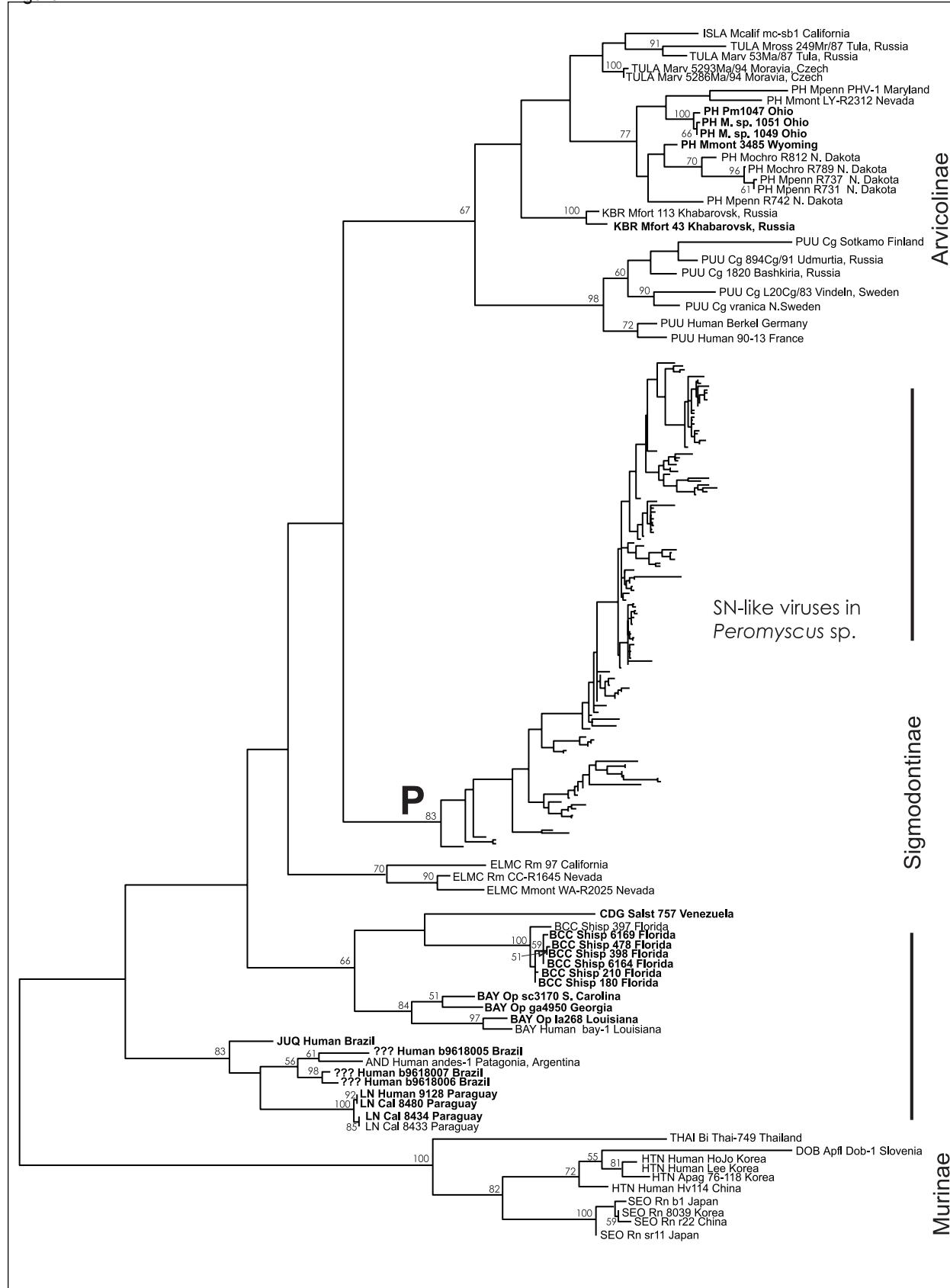


Figure 2

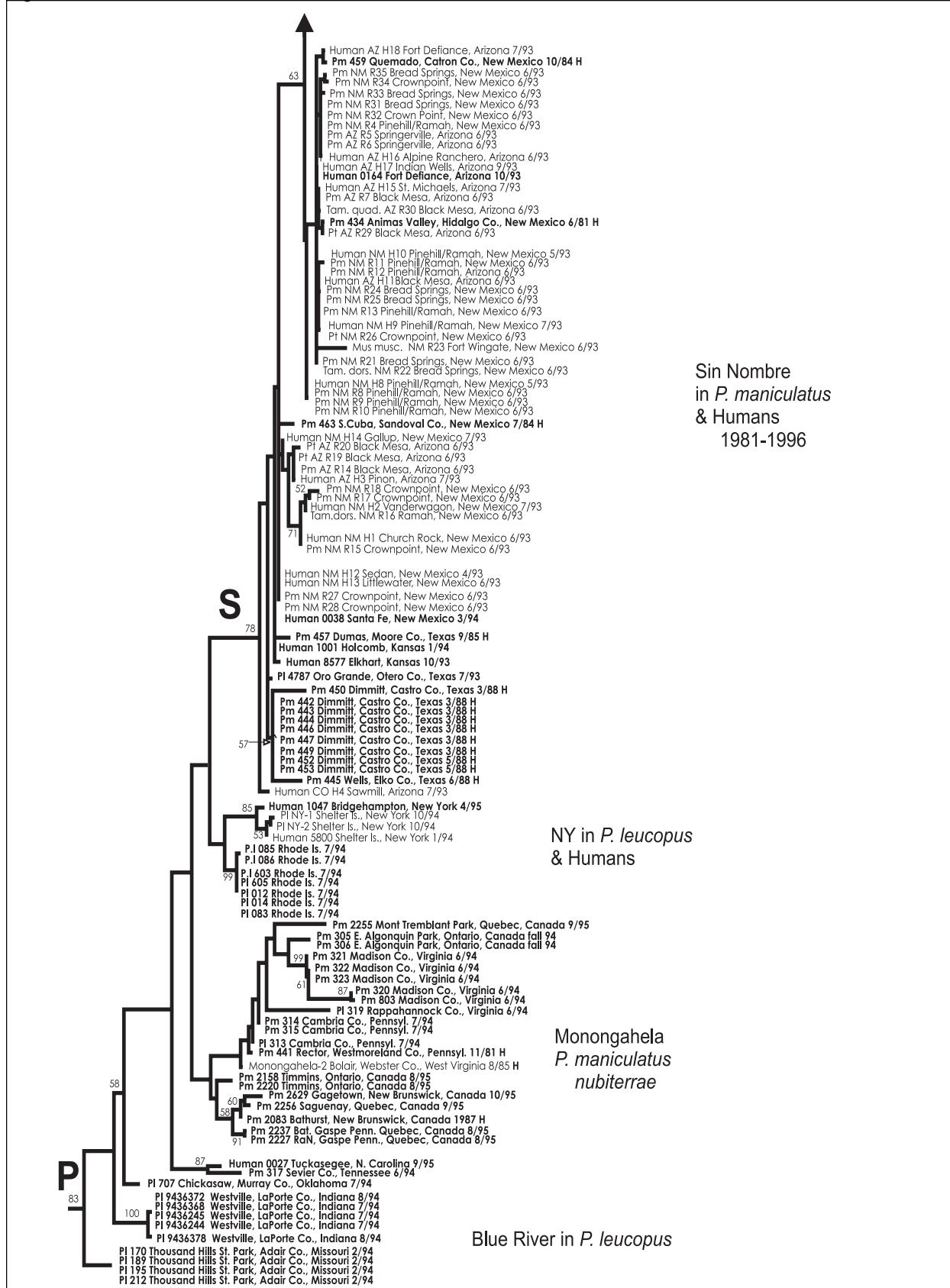


Figure 2, continued

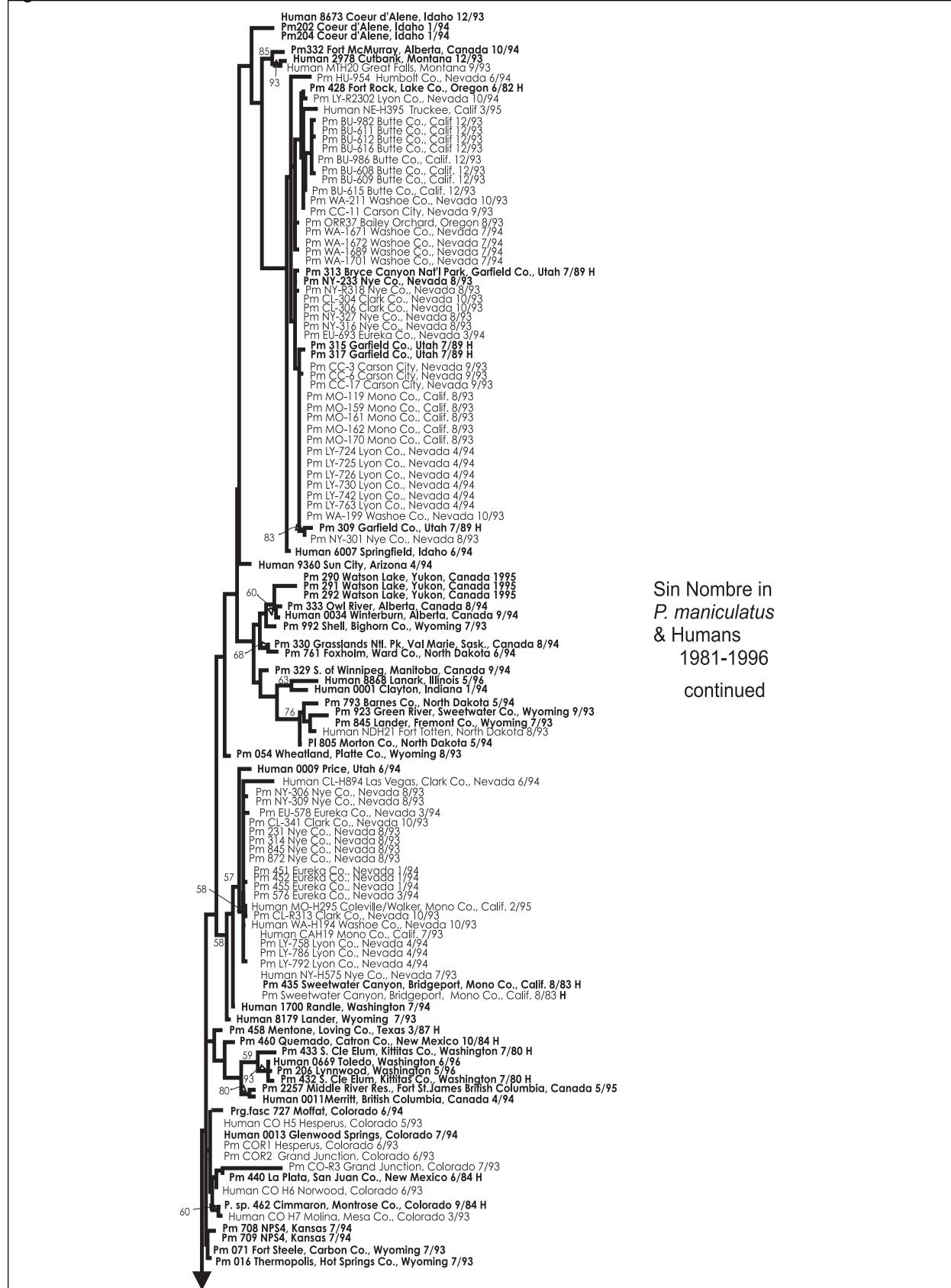


Figure 1. Overall hantavirus phylogenetic tree based on analysis of a 139 nucleotide fragment of the G2 coding region of the virus M segment. All newly reported sequences are shown bolded. The three virus groups corresponding to the hantaviruses carried by rodents of the subfamilies *Murinae*, *Sigmodontinae* and *Arvicolinae* are indicated. P indicates the clade containing the Sin Nombre-like viruses found in *Peromyscus* species rodents, the details of which are shown in figure 2. Horizontal branch lengths are proportional to the nucleotide step differences between taxa and predicted nodes. No scale bar is indicated as the actual number values are arbitrary due to the weighting used in the successive approximations method (see appendix for details). Bootstrap values greater than 50% are indicated above branches. Virus labels include the virus or virus lineage name (ISLA, Isla Vista; TULA, Tula; PH, Prospect Hill or Prospect Hill-like; KBR, Khabarovsk; PUU, Puumala; SN, Sin Nombre; ELMC, El Moro Canyon; CDG, Caño Delgadito; BCC, Black Creek Canal; BAY, Bayou; JUQ, Juquitiba; AND, Andes; LN, Laguna Negra; THAI, Thailand; DOB, Dobrava; HTN, Hantaan; SEO, Seoul), species source of material (Mcalif, *Microtus californicus*; Mross, *Microtus rossiaeemeridionalis*; Marv, *Microtus arvalis*; Mpenn, *Microtus pennsylvanicus*; Mmont, *Microtus montanus*, Mochro, *Microtus ochrogaster*; Mfort, *Microtus fortis*; Cg, *Clethrionomys glareolus*; Rm, *Reithrodontomys megalotis*; Salst, *Sigmodon alstoni*; Shisp, *Sigmodon hispidus*; Op, *Oryzomys palustris*; Cal, *Calomys laucha*; Bi, *Bandicota indica*; Apfl, *Apodemus flavicollis*; Apag, *Apodemus agrarius*; Rn *Rattus norvegicus*), identifier, and state, region or country of origin. A spreadsheet containing the details of all samples is available at <http://www.cdc.gov/eid>.

Figure 2. Phylogenetic tree of hantaviruses associated with *Peromyscus* species rodents. Figure provides a detailed view of clade P in figure 1. S indicates clade containing classical SN virus samples detected in humans or *P. maniculatus*. See figure 1 legend for overall tree description. Additional species source of material abbreviations include: Pm, *Peromyscus maniculatus*; Pl, *Peromyscus leucopus*, Prg.fasc, *Perognathus fasciatus*; Tam.quad, *Tamias quadrimaculatus*; Pt, *Peromyscus truei*; Mus musc., *Mus musculus*, and Tam.dors., *Tamias dorsalis*. Samples from historic materials are followed by an H.

the corresponding clades (13). Bootstrap values of 70% or higher corresponded to a probability of 95% or higher that the corresponding clade was correctly identified. Values of 50% or lower corresponded to a probability of 65% or lower that the clade was correctly identified (13).

Diversity of New World Hantaviruses

As expected on the basis of earlier nucleotide sequence analysis of a limited number of complete S or M hantavirus genome segments or virus genome fragments (5), the evolutionary relationships among hantaviruses were closely correlated with those of their known or suspected primary rodent reservoirs (Figure 1; Table 1). Hantaviruses associated with subfamily *Murinae* rodents (Hantaan, Dobrava, Seoul, and Thailand viruses) are clearly separated from those associated with *Arvicolinae* and *Sigmodontinae* rodents. The *Arvicolinae*-associated viruses (Puumala, Khabarovsk, Tula, Isla Vista, Prospect Hill [PH], and PH-like viruses) form a reasonably well-supported clade, but the phylogenetic position of this group relative to the *Murinae*- and *Sigmodontinae*-associated viruses is not well resolved.

The New World hantaviruses of the *Arvicolinae* group, primarily associated with *Microtus* species voles, include not only the classic PH virus (labeled PHV-1), originally isolated from *M. pennsylvanicus* in Maryland (14,15), and two other distinct PH-like virus lineages recently found in this vole species in North Dakota (R737 and R731; R742), but also Isla Vista virus in *M. californicus*, PH-like hantavirus lineages in *M. ochrogaster* in North Dakota (R812 and R789), and *M. montanus* in Wyoming and Nevada (3485; LY-R2312) (16,17). Virus phylogenetic placement is not clearly correlated with *Microtus* species of origin, indicating that either spill-over infection or host switching may occur with these viruses. An apparent example exists in the Ohio rodent samples of spill-over of a PH-like virus infection from *Microtus* species rodents to a deer mouse *Peromyscus maniculatus* (Pm1047). These viruses have not been associated with HPS cases.

The viruses associated with the subfamily *Sigmodontinae* rodents are highly diverse and are made up of several distinct viruses and lineages in North and South America. All viruses associated with *Peromyscus* species rodents form a well-supported distinct monophyletic clade

(labeled P in Figure 1); these viruses constitute the major cause of HPS cases in North America. Other HPS-associated viruses in this group include Black Creek Canal virus, associated with *Sigmodon hispidus*. This virus, the cause of a single HPS case, has been genetically detected in cotton rats throughout southern Florida but, so far, nowhere else in the United States. Another genetically distinct virus, Muleshoe virus, has been identified in *S. hispidus* from the western part of its range (18), but sequences were not available for comparison at the time of our analysis. Caño Delgadito virus, found in *S. alstoni* in Venezuela (19), appears to be monophyletic with Black Creek Canal viruses. However, bootstrap support for this relationship is low (lower than 50%). Reasonable support is found for the clade containing both these *Sigmodon* sp.-associated viruses and the Bayou viruses, present in *Oryzomys palustris* throughout the southeastern United States from the Atlantic coast to Texas (20-22). Bayou viruses have been associated with three HPS cases (20,22). El Moro Canyon virus has been found in numerous harvest mice (*Reithrodontomys megalotis*) throughout the southwestern United States but has also been found in other rodents (e.g., WA-R2025, in *M. montanus*), presumably indicating spill-over infections (16,18,23,24). So far, these viruses have not been associated with human disease. The current phylogenetic analysis places these viruses in a distinct supported clade.

We analyzed hantaviruses that are also associated with HPS cases in South America and form a well-supported clade that encompasses viruses from Brazil, Argentina, and Paraguay, including the original Juquitiba virus detected in a human autopsy sample from an HPS patient in Brazil in 1993 (25-27). The rodent host for this virus is unknown. Two additional hantavirus lineages have been detected in more recent Brazilian HPS cases (Johnson and Nichol, unpub. data), suggesting that at least three genetically distinct hantaviruses are associated with HPS cases in Brazil. One of these lineages (b9618005) is phylogenetically closer to the Andes virus found in Argentina (28). Andes virus has recently been associated with several HPS cases in Patagonia; its likely host is *Oligoryzomys longicaudatus* (5,28,29). Finally, Laguna Negra viruses form a well-supported monophyletic lineage. This virus, associated with a large HPS

outbreak in the Chaco region of Paraguay, is found in *Calomys laucha* rodents (10,30).

SNV-Like Viruses of *Peromyscus* Species Rodents

We analyzed 229 SNV-like viruses associated with *Peromyscus* species rodents; they form a well-supported (83%) clade (labeled P in Figure 1; details shown in Figure 2) and are distinct from other *Sigmodontinae*-associated hantaviruses. These SNV-like viruses include many classic SNVs, which are the major causes of HPS cases throughout the western and central United States and Canada, and are primarily associated with *P. maniculatus*. These viruses form a distinct, well-supported (78%) clade (labeled S in Figure 2), separate from other SNV-like viruses (Figure 2). Classic SNV 139 bp G2 fragments show up to an 18% nucleotide sequence divergence. Despite a number of exceptions, different genetic variants of SNV are grouped, generally speaking, by geography—an approximate geographic progression is apparent from the north and west toward the south and east, from the top of the tree down toward the node connecting these SNVs (labeled S in Figure 2). For instance, all samples from western Canada, including the Yukon, British Columbia, Alberta, Saskatchewan, and Manitoba are in the upper portion of this clade; two major lineages in California and Nevada (16,31) are also in this clade region. The lower part of the clade is dominated by viruses associated with the original Four Corners outbreak (New Mexico, Colorado, Utah, and Arizona) and other viruses from the Southwest, such as Kansas and Texas. Human HPS cases are represented throughout the SNV clade, indicating that these SNV variants can be associated with HPS illness.

In addition to recent samples, 30 SNV-like virus samples from the 1980s were included in the analysis to examine stability of the various SNV genetic lineages and their distribution (labeled H in Figure 2). Only small numbers of nucleotide differences, if any, were observed between old and recent virus sequences from the same geographic areas. The most striking example is the detection of identical viral G2 fragment sequences in rodents captured 12 years apart in New Mexico (Pm434) and Arizona (Pt AZ R29). Similarly, identical viral G2 sequences were found in rodents captured in eastern California in 1983 (our Pm435 and the previously

published Sweetwater Canyon sequence [32]) and in human and rodent materials from eastern California and western Nevada sampled 10 or more years later (e.g., Humans CAH19 and NY-H575, and Pm LY-758, 786, and 792). Other examples include 1 of 139 and 2 of 139 nucleotide sequence differences between Washington rodent Pm432 (captured in 1980) and Pm206 and HPS case 0669 (sampled 16 years later), respectively; only 2 of 139 nucleotides are different between Pm428 from southern Oregon and Pm LY-R2302 from northern Nevada, despite capture 12 years apart. These and other data (6,7,32,33) suggest that SNV has been present in North America for a considerable time and has been relatively stably maintained in rodent populations.

The next most closely related viruses are those detected in the northeastern United States, referred to as New York virus (34). These viruses have been detected in two human HPS cases and in *P. leucopus* in New York and Rhode Island (Figure 2). The 139 nucleotide fragments of these viruses have up to 10.1% nucleotide variation, and they differ from classic SNVs by at least 11.5% at the nucleotide level. The next closest group contains viruses associated with several "forest form" subspecies of *P. maniculatus* throughout the eastern United States and Canada, including the cloudland deer mouse (*P. maniculatus nubiterrae*), which inhabits the Appalachian mountain region (35). These viruses can also be found in some *P. leucopus* in this region (e.g., rodent Pl 313 from Pennsylvania). Up to 17.3% nucleotide variation can be seen among the 139 nucleotide fragments of these viruses. The name Monongahela has been suggested for this virus lineage (36), which differs from New York and SN viruses by at least 8.6% and 10.8% nucleotide differences, respectively. Another distinct hantavirus lineage can be seen in *P. maniculatus* in Tennessee and has been associated with an HPS case (0027) in eastern North Carolina. These viruses are 7.9% different from one another at the nucleotide level for the 139 nucleotide fragment analyzed, and at least 12.2%, 14.4%, and 15.8% different from New York, Monongahela, and SN virus lineages, respectively. Additional distinct virus lineages, recently referred to as Blue River virus (37), can be detected in *P. leucopus* in Oklahoma (Pl 707), Indiana (e.g., Pl 9436372 and Pl 9436378), and Missouri (e.g., Pl 170). The Oklahoma lineage

virus is 10.1%, 10.8%, 15.8% different from the viruses in the Missouri, Indiana, and Tennessee lineages.

In addition to identifying the distinct SNV-like viruses and virus genetic lineages throughout North America, our study provides data suggesting the likely site of infection and minimum incubation time for some HPS cases. As reported earlier (2), the HPS case labeled CO H5 was originally described as an Arizona case because the person was residing near Springerville, Arizona, when the illness began. However, the person had been living in Hesperus, Colorado, 11 days before disease onset. The PCR fragment amplified from the case autopsy specimen and from the *P. maniculatus* trapped at the household in Hesperus matched exactly and differed from those amplified from *P. maniculatus* in the Arizona location (Figure 2). Similarly, a patient (labeled human 0038) whose symptoms began in Los Angeles, California, had been in the Santa Fe, New Mexico, area 28 to 35 days before illness onset. Analysis of PCR fragments linked the source of infection to New Mexico, rather than to California (Figure 2).

Virus and Host Genetic Relationships and Evolution

The genetic data we present indicate a broad spectrum of genetic variants of SNV-like viruses throughout North America, associated primarily with *Peromyscus* rodents. Recent analysis of rodent mitochondrial DNA sequence differences suggests that the different SNV-like virus lineages are primarily associated with different *Peromyscus* species, and in some cases, with phylogenetically distinct subspecies or mitochondrial DNA haplotypes (Morzunov and Nichol, unpub. data; 37). For instance, the classic SNV and the Monongahela virus lineages are found associated with the "grassland form" and "forest form" of *P. maniculatus*, respectively (they represent different subspecies and appear phylogenetically distinct with respect to their mitochondrial DNA [Morzunov and Nichol, unpub. data]). The New York virus, and the Blue River virus lineages found in Indiana and Oklahoma, appear associated with genetically distinct *P. leucopus* populations (37). This pattern likely reflects microadaptation of the virus to the rodent host and not just geographic isolation of the virus variants. This view is supported by the observation that even in areas

such as the eastern United States (particularly the Appalachian Mountain region), where *P. maniculatus* (forest form) and *P. leucopus* (eastern form) are sympatric and share microhabitat, extensive virus mixing between species is not seen; the Monongahela virus lineage is found predominantly in *P. maniculatus*, and the New York virus lineage in *P. leucopus*. Such data suggest that the broad correlation clearly evident between virus evolutionary relationships and those of their primary rodent reservoirs likely exists even at the finer level of closely related species and subspecies. However, the fact that the *P. leucopus*-associated New York virus appears phylogenetically closer to the *P. maniculatus*-associated viruses (SN and Monongahela) than to other *P. leucopus*-associated viruses (Blue River) suggests that this coevolutionary relationship is not absolute and that some species jumping (host-switching) may also have occurred. While the exact phylogenetic relationship of the SNV lineages to Monongahela, New York, and the other *P. leucopus* virus lineages is not well resolved by using the 139-bp G2 fragment we analyzed, analysis of more complete sequence data strongly supports a similar topology, placing New York virus firmly within the clade of *P. maniculatus*-borne viruses (37). This evidence, together with significant spill-over infection that sometimes occurs between sympatric rodents, illustrates the complexity of the hantavirus-host interactions.

This observation leads into another area of complexity, namely, the definition of distinct hantavirus serotypes or species. In the past, a newly identified arbovirus would be considered a distinct virus or virus serotype if a fourfold or greater two-way difference between this virus and previously recognized closely related viruses was obtained in virus neutralization assays. Despite the obvious biologic limitation (a single amino acid change can allow virus to escape from neutralization), this traditional criterion correlates remarkably well with more recent molecular data. One problem is that hantaviruses are generally difficult to isolate in tissue culture and are frequently noncytopathic, often making plaque assay analysis impractical (Table 1).

An attempt to define distinct virus species by using more widely used general criteria for the definition of biologic species is under way. Most defined species could be described as the lowest taxonomic unit that is geographically and

ecologically contained, reproductively isolated, phylogenetically distinct, and self-sufficient. The apparent long-term maintenance and coevolution of phylogenetically distinct hantaviruses with different primary rodent reservoir species provides a foundation on which to build a hantavirus species definition. That is, if little host switching has occurred and if instead hantaviruses are associated with specific primary rodent reservoir species for many thousands of years, identification of a hantavirus in a unique primary rodent reservoir species would strongly suggest that in further analyses (e.g., nucleotide and amino acid sequence, cross-neutralization), it will be found to represent a new virus species. Hantaviruses maintained in rodent hosts from different genera (e.g., SNV in *Peromyscus* species rodents compared with Black Creek Canal virus in *Sigmodon* species rodents) will clearly meet the broad criteria for separate species status. This view is reinforced by recent data showing that stable reassortant viruses of different SNV genetic lineages can be readily detected in nature (31,38) and in tissue-culture mixed infections (39), but not in virus pairs such as SNV and Black Creek Canal virus (39). Difficulty can arise when trying to determine the species status of viruses maintained within rodent hosts of the same genera or species. So far, SN, New York, Monongahela, and Blue River viruses have been suggested as distinct hantaviruses with independent species names (5,36,37). The genetic analysis we present suggests that, as more hantavirus-infected *Peromyscus* species samples are analyzed, it is increasingly difficult to draw clear lines separating these virus species. The decision regarding whether to lump these viruses together as SNV-like viruses or to split them into separate species status will require the availability of neutralization data for several representatives of each virus, more detailed identification of the virus-host relationships, and more complete genetic characterization of both viruses and their hosts.

Appendix

Rodent and HPS Case Materials

The newly described nucleotide sequences were derived from rodent materials collected as part of a nationwide survey of rodents for hantavirus antibodies (Ksiazek et al., unpub. data). Most of the

human HPS-case blood and tissue autopsy samples were obtained and examined during the original investigation of an HPS outbreak in the Four Corners area of the southwestern United States in 1993 and as part of national surveillance for hantavirus disease throughout the United States from 1993 to 1997. Canadian rodent and HPS case materials were provided by the Laboratory Centre for Disease Control, Canada. Historic rodent samples were obtained from the Division of Biological Materials of the Museum of Southwestern Biology (Albuquerque, NM), University of New Mexico.

RNA Extraction, RT-PCR Amplification and Sequencing

Total RNA was extracted from human and rodent tissues, blood, or serum (2,10). Because of the hazardous nature of the virus, homogenization of rodent and human autopsy materials and extraction of RNA were performed in a certified class IIb laminar flow biosafety hood in Biosafety Level 3 containment. RNA was extracted from tissue or blood products by using acid guanidinium thiocyanate and phenol-chloroform and purified by using the RNaid Kit (Bio 101, La Jolla, CA). Nested RT-PCR assays were used to amplify DNA products containing a small fragment of the G2 coding region of M segment (2,10). Rodent and human samples were amplified separately, and all manipulations that might result in possible cross-contamination of samples were avoided. PCR products of correct size were sequenced with the same primers used for second-round PCR amplification in conjunction with various generations of sequencing kits available from Applied Biosystems, Inc. (Perkin Elmer, Foster City, CA). Sequences 139

nucleotides in length determined from each PCR product were used in phylogenetic analysis.

Oligonucleotide Primer Design

Oligonucleotide primers were used to generate DNA fragments from the G2 region of hantavirus M RNA (Table 2). In the initial phase of this project, amplification of hantavirus sequences from autopsy tissues of fatal HPS cases and hantavirus antibody-positive rodents in the southwestern United States used primers designed on the basis of nucleotide sequences conserved among PH and Puumala viruses (2). On the basis of SNV nucleotide sequences derived from these materials, new primers were designed and optimized for detection of SNV-like viruses associated with *P. maniculatus* (11). As more sequence data became available, additional generations of primers were refined that would detect hantaviruses from other geographic regions of the United States. The development of broadly reactive primers designed to detect hantaviruses associated with subfamily *Sigmodontinae* rodents (10) has eliminated the effort of amplifying RNA samples with many sets of primers.

Nucleotide Sequence and Phylogenetic Analyses

Compilation, alignment, and comparative nucleotide sequence analysis was carried out by using the Wisconsin Sequence Analysis Package, version 8.1 (Genetics Computer Group, Inc., Madison, WI) on a DEC 3000-500X AXP workstation (Digital Equipment Corp., Maynard, MA). Phylogenetic analysis was performed by maximum parsimony analysis using PAUP version 4.0 d52 (12) on a Power PC 9500. The size and complexity of the dataset prevented the

Table 2. PCR and sequencing primers

1st-round primers (5' to 3')	2nd-round primers (5' to 3')	Basis of primer design (ref.)	Amplicon size
TTAAGCAATGGTG(C/T)ACTAC(T/A)AC	AGAAAGAAATGTGCATTG C	Puumala/Prospect Hill/ <i>Arvicolineae</i> (2)	278
CCATAACACAT(A/T)GCAGC	CCTGAACCCCATGC(A/T/C)CCATC		
TTAAGCAATGGTG(C/T)ACTAC(T/A)AC	AAGGTAACACAGT(G/C)TCTGGATTC	Sin Nombre/Western	185
CCATAACACAT(A/T)GCAGC	GGTTATCACTTAGATC(C/T)TGAAAGG	U.S. 1st generation (2)	
AGAAAGATCTGGGGTTGC	AAGGTAACACAGT(G/C)TCTGGATTC	Sin Nombre/Western	185
CCTGAACCCCAGGCCCGT	GGTTATCACTTAGATC(C/T)TGAAAGG	U.S. 2nd generation (11)	
TGTGTGTTGGAGACCTGG	ATGTCAACAAC(A/G)AGTGGGATG	Sin Nombre Nevada/	185
TC(A/G)ATAGATTGTGTATGCA	CATGGGTTATCACTTAG(G/A)TC	E. California (31)	
CAGAAAGATCTGGGGTTGC	CAAGGGAATACTGTCTGGATTT		
CCCGAGCCCCATGCACCAC	GATTGTCACTCAGATCTGAAATG	Bayou virus/LA/ East Coast/ S. American (19,20)	185
TGTGAITATCAAGGIAAIAC	TGTGAITATCAAGGIAAIAC	General <i>Sigmodontinae</i>	242
ACIG(A/T)IGCICCATAICACAT	CCCCAIGCICCICTCAAT	(10)	

use of branch and bound search method and weighting of the data matrix based on transition:transversion bias. Maximum parsimony analysis of the hantavirus G2 fragment nucleotide sequences was carried out by using the heuristic search option. The initial unweighted analysis showed considerable homoplasy within the dataset. A successive approximations method was used in which characters were weighted by using the maximum value of their rescaled consistency index (12), and the heuristic search repeated. Bootstrap analysis was carried out by 500 replicates of the heuristic search with random resampling of the data. The analysis required several months of computer time; thus, it was not possible to include some recently published additional hantaviruses sequences. The nucleotide sequence dataset (bigtree.nex) we used is available in NEXUS format (compatible with most phylogenetic analysis software packages) accessible through the journal website (<http://www.cdc.gov/eid>). A brief description of all samples analyzed (bigtree.exl in EXCEL 2.1 spreadsheet format), and the phylogenetic tree of Figures 1 and 2 can also be found at the same location on the website.

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References

- McKee Jr KT, LeDuc JW, Peters CJ. Hantaviruses. In: Belshe RB, editor. *Textbook of human virology*. 2nd ed. St. Louis (MO): Mosby; 1991. p. 615-32.
- Nichol ST, Spiropoulou CF, Morzunov SP, Rollin PE, Ksiazek TG, Feldmann H, et al. Genetic identification of a hantavirus associated with an outbreak of acute respiratory illness. *Science* 1993;262:914-7.
- Childs JE, Ksiazek TG, Spiropoulou CF, Krebs JW, Morzunov S, Maupin GO, et al. Serologic and genetic identification of *Peromyscus maniculatus* as the primary rodent reservoir for a new hantavirus in the southwestern United States. *J Infect Dis* 1994;169:127-80.
- Duchin JS, Koster FT, Peters CJ, Simpson GL, Tempest B, Zaki SR, et al. Hantavirus pulmonary syndrome: a clinical description of 17 patients with a newly recognized disease. *N Engl J Med* 1994;330:949-55.
- Schmaljohn C, Hjelle B. Hantaviruses: a global disease problem. *Emerg Infect Dis* 1997;3:95-104.
- Tsai TF, Bauer SP, Sasso DR, Whitfield SG, McCormick JB, Caraway CT, et al. Serological and virological evidence of a Hantaan virus-related enzootic in the United States. *J Infect Dis* 1985;152:126-36.
- Yanagihara R, Daum CA, Lee P-W, Baek L-J, Amyx HL, Gajdusek DC, et al. Serological survey of Prospect Hill virus infection in indigenous wild rodents in the USA. *Trans R Soc Trop Med Hyg* 1987;81:42-5.
- Mills JN, Johnson JM, Ksiazek TG, Ellis BA, Rollin PE, Yates TL, et al. A survey of hantavirus antibody in small-mammal populations in selected United States national parks. *Am J Trop Med Hyg* 1998;58:525-32.
- Mills JN, Johnson JM, Ksiazek TG, Ellis BA, Rollin PE, Yates TL, et al. A survey of hantavirus antibody in small-mammal populations in selected United States national parks. *Am J Trop Med Hyg* 1998;58:525-32.
- Johnson AM, Bowen MD, Ksiazek TG, Williams RJ, Bryan RT, Mills JN, et al. Laguna Negra virus associated with HPS in western Paraguay and Bolivia. *Virology* 1997;238:115-27.
- Spiropoulou CF, Morzunov S, Feldmann H, Sanchez A, Peters CJ, Nichol ST. Genome structure and variability of a virus causing hantavirus pulmonary syndrome. *Virology* 1994;200:715-23.
- Swofford DL. PAUP*: phylogenetic analysis using parsimony (*and other methods) [computer program]. Version 4.0. Sinauer, Sunderland, MA; 1998.
- Hillis DM, Bull JJ. An empirical test of bootstrapping as a method for assessing confidence in phylogenetic analysis. *Syst Biol* 1993;42:182-92.
- Lee P, Amyx HL, Yanagihara R, Gajdusek DC, Goldgaber D, Gibbs Jr CJ. Partial characterization of Prospect Hill virus isolated from meadow voles in the United States. *J Infect Dis* 1985;152:826-9.
- Parrington MA, Lee PW, Kang CY. Molecular characterization of the Prospect Hill virus M RNA segment: comparison with the M RNA segments of other hantaviruses. *J Gen Virol* 1991;72:1845-54.
- Rowe JE, St Jeor SC, Riolo J, Otteson EW, Monroe MC, Ksiazek TG, et al. Coexistence of several novel hantaviruses in rodents indigenous to North America. *Virology* 1995;213:122-30.
- Song W, Torrez-Martinez N, Irwin W, Harrison FJ, Davis R, Ascher M, et al. Isla Vista virus: a genetically novel hantavirus of the California vole *Microtus californicus*. *J Gen Virol* 1995;76:3195-9.
- Rawlings JA, Torrez-Martinez N, Neill SU, Moore GM, Hicks BN, Pichuantes S, et al. Cocirculation of multiple hantaviruses in Texas, with characterization of the small (S) genome of a previously undescribed virus of cotton rats (*Sigmodon hispidus*). *Am J Trop Med Hyg* 1996;55:672-9.
- Fulhorst CF, Monroe MC, Salas RA, Duno G, Utrera A, Ksiazek TG, et al. Isolation, characterization, and geographic distribution of Caño Delgadito virus, a newly discovered South American hantavirus (family Bunyaviridae). *Virus Res* 1997;51:159-71.

20. Morzunov SP, Feldmann H, Spiropoulou CF, Semenova VA, Rollin PE, Ksiazek TG, et al. A newly recognized virus associated with a fatal case of hantavirus pulmonary syndrome in Louisiana. *J Virol* 1995;69:1980-3.
21. Ksiazek TG, Nichol ST, Mills JN, Groves MG, Wozniak A, McAdams S, et al. Isolation, genetic diversity and geographic distribution of Bayou virus. *Am J Trop Med Hyg* 1997;57:445-8.
22. Hjelle B, Goade D, Torrez-Martinez N, Lang-Williams M, Kim J, Harris RL, et al. Hantavirus pulmonary syndrome, renal insufficiency and myositis associated with infection by Bayou hantavirus. *Clin Infect Dis* 1996;23:495-500.
23. Hjelle B, Chavez-Giles F, Torrez-Martinez N, Yates T, Sarisky J, Webb J, et al. Genetic identification of a novel hantavirus of the harvest mouse *Reithrodontomys megalotis*. *J Virol* 1994;68:6751-4.
24. Torrez-Martinez N, Song W, Hjelle B. Nucleotide sequence analysis of the M genomic segment of El Moro Canyon hantavirus: antigenic distinction from Four Corners hantavirus. *Virology* 1995;211:336-8.
25. Nichol ST, Ksiazek TG, Rollin PE, Peters CJ. Hantavirus pulmonary syndrome and newly described hantaviruses in the United States. In: Elliott RM, editor. *The Bunyaviridae*. New York: Plenum Press; 1996. p. 269-80.
26. da Silva MV, Vasconcelos MJ, Hidalgo NTR, Veiga APR, Canzian M, Marotto PCF, et al. Rev Ins Med Trop Sao Paulo 1997;39:231-4.
27. Vasconcelos MJ, Lima VP, Iversson LB, Rosa MDB, Travassos Da Rosa APA, Travassos Da Rosa ES, et al. Pulmonary syndrome in the rural area of Juquitiba, São Paulo metropolitan area, Brazil. *Rev Inst Med Trop Sao Paulo* 1997;39:237-8.
28. Lopez N, Padula P, Rossi C, Lazaro ME, Franze-Fernandez MT. Genetic identification of a new hantavirus causing severe pulmonary syndrome in Argentina. *Virology* 1996;220:223-6.
29. Levis S, Rowe JE, Morzunov S, Enria DA, St Jeor S. New hantavirus causing hantavirus pulmonary syndrome in central Argentina. *Lancet* 1997;349:998-9.
30. Williams RJ, Bryan RT, Mills JN, Palma RE, Vera I, de Velasquez F, et al. An outbreak of hantavirus pulmonary syndrome in western Paraguay. *Am J Trop Med Hyg* 1997;57:274-82.
31. Henderson WW, Monroe MC, St Jeor SC, Thayer WP, Rowe JE, Peters CJ, et al. Naturally occurring Sin Nombre virus genetic reassortants. *Virology* 1995;213:602-10.
32. Nerurkar VR, Song JW, Song KJ, Nagle JW, Hjelle B, Jenison S, et al. Genetic evidence for a hantavirus enzootic in deer mice (*Peromyscus maniculatus*) captured a decade before the recognition of hantavirus pulmonary syndrome. *Virology* 1994;204:563-8.
33. Zaki SR, Khan AS, Goodman RA, Armstrong LR, Greer PW, Coffield LM, et al. Retrospective diagnosis of hantavirus pulmonary syndrome, 1978-1993—Implications for emerging infectious diseases. *Arch Path Lab Med* 1996;120:134-9.
34. Hjelle B, Lee SW, Song W, Torrez-Martinez N, Song JW, Yanagihara R, et al. Molecular linkage of hantavirus pulmonary syndrome to the white-footed mouse, *Peromyscus leucopus*: genetic characterization of the M genome of New York virus. *J Virol* 1995;69:8137-41.
35. Hall ER. *Mammals of North America*. New York: John Wiley and Sons; 1981.
36. Song JW, Baek LJ, Nagle JW, Schlitter D, Yanagihara R. Genetic and phylogenetic analyses of hantaviral sequences amplified from archival tissues of deer mice (*Peromyscus maniculatus nubiterrae*) captured in the eastern United States. *Arch Virol* 1996;141:959-67.
37. Morzunov SP, Rowe JE, Ksiazek TG, Peters CJ, St Jeor SC, Nichol ST. Genetic analysis of the diversity and origin of hantaviruses in *Peromyscus leucopus* mice in North America. *J Virol* 1998;72:57-64.
38. Schmaljohn AL, Li D, Negley DL, Bressler DS, Turell MJ, Korch GW, et al. Isolation and initial characterization of a new found hantavirus from California. *Virology* 1995;206:963-72.
39. Rodriguez LL, Owens JH, Peters CJ, Nichol ST. Genetic reassortment among viruses causing hantavirus pulmonary syndrome. *Virology* 1998;242:99-106.

number	virus sample order in figs. 1 and 2	labels in eid.nex	genbank	sequence 2	sequence 3	sequence 4	sequence 5	sequence 6	sequence 7	sequence 8	sequence 9	sequence 10	sequence 11	sequence 12
1	ISLA Mcalif mc-sb1 California	lvu3153	U21633	ISLA Mcalif mc-sb47 California (cvu19304)										
2	TULA Mar9 249M/93 Tula, Russia	ulm249	Z48975											
3	TULA Marv 53Mar/94 Tula, Russia	ulmmor93	Z48976											
4	TULA Marv 53Mar/94 Moravia, Czech	ulmmor93	Z48977											
5	TULA Marv 538Mar/94 Moravia, Czech	ulvm89m	Z66538											
6	PH Mpenn PHV-1 Maryland	phvmsma	X55129											
7	PH Mmont LY-R2312 Nevada	phv33240	U33240											
8	PH Pmt1047 Ohio	pm1047oh												
9	PH M. sp. 1051 Ohio	r1051oh												
10	PH M. sp. 1049 Ohio	r1049oh												
11	PH Mmont 3485 Wyoming	mm3485wy												
12	PH Mucho R812 N. Dakota	phu33254	U33254											
13	PH Mucho R789 N. Dakota	phu33251	U33251											
14	PH Mpenn R737 N. Dakota	phu33247	U33247											
15	PH Mpenn R731 N. Dakota	phu33245	U33245											
16	PH Mpenn R742 N. Dakota	phu33256	U33256											
17	KBR Mfot 113 Khabarovsk, Russia	mf113												
18	KBR Mfot 43 Khabarovsk, Russia	khu35254	U35254											
19	PUU Cg Sotkamo Finland	puumgp	X61034											
20	PUU Cg 894Cg/91 Udmurtia, Russia	puumdpm	Z21509											
21	PUU Cg 1820 Bashkiria, Russia	puumseg	M29979											
22	PUU Cg L20Cg/83 Vindeln, Sweden	pumvmin83	Z49214											
23	PUU Cg vrancam N.Sweden	vranicam	U14136											
24	PUU Human Berkel Germany	puugp2n	L36944											
25	PUU Human 90-13 France	pvu22418	U22418											
26	ELMC Rm 97 California	emu66828	U26828											
27	ELMC Rm CC-R1645 Nevada	emu33225	U33225											
28	ELMC Mmont WA-R2025 Nevada	emu33260	U33260											
29	CDG Salst 757 Venezuela	vn757												
30	BCC Shisp 397 Florida	hvimega	L39950											
31	BCC Shisp 6169 Florida	f16169												
32	BCC Shisp 478 Florida	f1478												
33	BCC Shisp 398 Florida	f1398												
34	BCC Shisp 6164 Florida	f16164												
35	BCC Shisp 210 Florida	f210												
36	BCC Shisp 180 Florida	f1180												
37	BAY Op scs170 S. Carolina	9613170												
38	BAY Op ga4950 Georgia	rga4950												
39	BAY Op la268 Louisiana	rla268												
40	BAY Human bay-1 Louisiana	hvglyprie	L36930											
41	JUQ Human Brazil	brazil												
42	??? Human b9618005 Brazil	b9618005												
43	AND Human Andes-1 Patagonia, Argentina	andes												
44	??? Human b9618007 Brazil	b9618007												
45	??? Human b9618006 Brazil	b9618006												
46	LM Cal 4340 Paraguay	pg9128												
47	LM Cal 4340 Paraguay	pg94840												
48	LM Cal 4343 Paraguay	pg948434												
49	LM Cal 4343 Paraguay	pg94433												
50	THAI Bi Thai-749 Thailand	thai												
51	DOB Apfl Obc 1 Slovenia	L06756												
52	HTN Human Ho Korea	hnvdbsm	L33685											
53	HTN Human Lee Korea	htllee	D00377	HTN Human Ho Korea										
54	HTN Human 76-116 Korea	hanm	M14627											
55	HTN Human Hv114 China	htvh114	L08753											
56	SEO Rn b1 Japan	seob1	X53861											
57	SEO Rn 8039 Korea	see9039	S47716											
58	SEO Rn 8229 China	seor22	S68035											
59	SEO Rn sr11 Japan	seor11	M34882											
60	Human 8673 Coeur d'Alene, Idaho 1/93	id8673	Pm202 Coeur d'Alene, Idaho 1/94											
61	Pm202 Coeur d'Alene, Idaho 1/94													
62	Pm204 Coeur d'Alene, Idaho 1/94													
63	Pm332 Fort McMurray, Alberta, Canada 10/94	rcn332												
64	Human 2978 Cutbank, Montana 12/93	mt2978												
65	Human MT H20 Great Falls, Montana 9/93	pror	L27776											
66	Pm HU-954 Humbolt Co., Nevada 6/94	snu33238	U33238											
67	Pm 428 Fort Rock, Lake Co., Oregon 6/82	ror428												
68	Pm LY-R2302 Lyon Co., Nevada 10/94	snu33239	U33239											
69	Human NE-H395 Truckee, Calif 3/95	snu33445	U33445											
70	Pm BU-982 Butte Co., Calif 12/93	snu33223	U33223											
71	Pm BU-611 Butte Co., Calif 12/93	snu33221	U33221	Pm BU-612 Butte Co., Calif 12/93										
72	Pm BU-612 Butte Co., Calif 12/93													
73	Pm BU-616 Butte Co., Calif 12/93	snu33224	U33224											
74	Pm BU-986 Butte Co., Calif 12/93	snu33219	U33219	Pm BU-609 Butte Co., Calif. 12/93										
75	Pm BU-608 Butte Co., Calif 12/93													
76	Pm BU-609 Butte Co., Calif. 12/93													
77	Pm BU-615 Butte Co., Calif. 12/93	snu33222	U33222	Pm BU-616 Butte Co., Calif 12/93										
78	Pm WA-211 Washoe Co., Nevada 10/93	snu33262	U33262	Pm CC-11 Carson City, Nevada 9/93										
79	Pm CC-11 Carson City, Nevada 9/93													
80	Pm OR R37 Bailey Orchard, Oregon 8/93	proak	L27795											
81	Pm WA-1671 Washoe Co., Nevada 7/94	snu33257	U33257	Pm WA-1672 Washoe Co., Nevada 7/94										
82	Pm WA-1672 Washoe Co., Nevada 7/94													
83	Pm WA-1689 Washoe Co., Nevada 7/94													
84	Pm WA-1701 Washoe Co., Nevada 7/94													
85	Pm 313 Bryce Canyon Natl Park, Garfield Co. rut313													
86	Pm NY-233 Nye Co., Nevada 8/93	nvr233												
87	Pm NY-R318 Nye Co., Nevada 8/93	hvu44992	U44992											
88	Pm CL-304 Clark Co., Nevada 10/93	snu33229	U33229	Pm CL-306 Clark Co., Nevada 10/93										
89	Pm CL-306 Clark Co., Nevada 10/93													

90 Pm NY-327 Nye Co., Nevada 8/93					
91 Pm NY-316 Nye Co., Nevada 8/93					
92 Pm EU-693 Eureka Co., Nevada 3/94					
93 Pm 315 Garfield Co., Utah 7/89	rut315	Pm 317 Garfield Co., Utah 7/89			
94 Pm 317 Garfield Co., Utah 7/89					
95 Pm CC-3 Carson City, Utah 7/93	snu33227	U33227 Pm CC-6 Carson City, Nevada 9/93	Pm CC-17 Carson City, Nevada 9/93		
96 Pm CC-6 Carson City, Nevada 9/93					
97 Pm CC-17 Carson City, Nevada 9/93					
98 Pm MO-119 Mono Co., Calif. 8/93	prol	L27770 Pm MO-159 Mono Co., Calif. 8/93	Pm MO-161 Mono Co., Calif. 8/93	Pm MO-162 Mono Co., Calif. 8/93	Pm MO-171 Pm LY-724 L Pm LY-725 L Pm LY-726 Pm LY-730 Pm LY-742 L Pm LY-763 L Pm WA-199 Washoe Co., Nevada 10/93
99 Pm MO-159 Mono Co., Calif. 8/93					
100 Pm MO-161 Mono Co., Calif. 8/93					
101 Pm MO-162 Mono Co., Calif. 8/93					
102 Pm MO-170 Mono Co., Calif. 8/93					
103 Pm LY-724 Lyon Co., Nevada 4/94					
104 Pm LY-725 Lyon Co., Nevada 4/94					
105 Pm LY-726 Lyon Co., Nevada 4/94					
106 Pm LY-730 Lyon Co., Nevada 4/94					
107 Pm LY-742 Lyon Co., Nevada 4/94					
108 Pm LY-763 Lyon Co., Nevada 4/94					
109 Pm WA-199 Washoe Co., Nevada 10/93					
110 Pm 309 Garfield Co., Utah 7/89	rut309				
111 Pm NY-301 Nye Co., Nevada 8/93	hvu44991	U44991			
112 Human 6007 Springfield, Idaho 6/94	id6007				
113 Human 9360 Sun City, Arizona 4/94	az9360				
114 Pm 290 Watson Lake, Yukon, Canada 1995	yukon		Pm 291 Watson Lake, Yukon, Canada 1995	Pm 292 Watson Lake, Yukon, Canada 1995	
115 Pm 291 Watson Lake, Yukon, Canada 1995					
116 Pm 292 Watson Lake, Yukon, Canada 1995					
117 Pm 333 Owl River, Alberta, Canada 8/94	rcn333				
118 Human 0034 Winterburn, Alberta, Canada 9/94	hc034				
119 Pm 992 Shell, Bighorn Co., Wyoming 7/93	wy28992				
120 Pm 330 Grasslands Nt. Pk, Val Marie, Sask.,	rcn330				
121 Pm 761 Foxholm, Ward Co., North Dakota 6/94	nd761				
122 Pm 329 S. of Winnipeg, Manitoba, Canada 9/9	rcn329				
123 Human 8688 Lanark, Illinois 5/96	9608688m				
124 Human 0001 Clayton, Indiana 1/94	ind				
125 Pm 793 Barnes Co., North Dakota 5/94	ndf793				
126 Pm 923 Green River, Sweetwater Co., Wyoming 28923		Pm 845 Lander, Fremont Co., Wyoming 7/93			
127 Pm 845 Lander, Fremont Co., Wyoming 7/93		L27777			
128 Human ND H21 Fort Totten, North Dakota 6/93	pros				
129 PI 805 Morton Co., North Dakota 5/94	ndr805				
130 Pm 054 Wheatland, Platte Co., Wyoming 8/93	wy29054				
131 Human 0009 Price, Utah 6/94	ut0009				
132 Human CL-H894 Las Vegas, Clark Co., Nevada 3/94	snu33233				
133 Pm NY-306 Nye Co., Nevada 8/93	nvr0609	U45023	Pm NY-309 Nye Co., Nevada 8/93	Pm 845 Nye Co., Nevada 8/93	Pm 872 Nye Co., Nevada 8/93
134 Pm NY-309 Nye Co., Nevada 8/93					
135 Pm EU-578 Eureka Co., Nevada 3/94	snu33236	U33236			
136 Pm CL-341 Clark Co., Nevada 10/93	snu33231	U33231	Pm 231 Nye Co., Nevada 8/93	Pm 314 Nye Co., Nevada 8/93	Pm 845 Nye Co., Nevada 8/93
137 Pm 231 Nye Co., Nevada 8/93					
138 Pm 314 Nye Co., Nevada 8/93					
139 Pm 845 Nye Co., Nevada 8/93					
140 Pm 872 Nye Co., Nevada 8/93					
141 Pm 451 Eureka Co., Nevada 1/94	snu33234	U33234	Pm 452 Eureka Co., Nevada 1/94	Pm 455 Eureka Co., Nevada 1/94	Pm 576 Eureka Co., Nevada 3/94
142 Pm 452 Eureka Co., Nevada 1/94					
143 Pm 455 Eureka Co., Nevada 1/94					
144 Pm 576 Eureka Co., Nevada 3/94					
145 Human MO-H295 Coleville/Walker, Mono Co.,	snu33244	U33244			
146 Pm CL-R313 Clark Co., Nevada 10/93	snu33230	U33230			
147 Human WA-H194 Washoe Co., Nevada 10/93	snu33264	U33264			
148 Human CA H19 Mono Co., Calif. 7/93	prok	L27769	Pm LY-758 Lyon Co., Nevada 4/94	Pm LY-786 Lyon Co., Nevada 4/94	Pm LY-792 Lyon Co., Nevada 4/94
149 Pm LY-758 Lyon Co., Nevada 4/94					
150 Pm LY-786 Lyon Co., Nevada 4/94					
151 Pm LY-792 Lyon Co., Nevada 4/94					
152 Human NY-H575 Nye Co., Nevada 7/93					
153 Pm 435 Sweetwater Canyon, Bridgeport, Mono Co., Calif. 8/83					
154 Pm Sweetwater Canyon, Bridgeport, Mono Co., Calif. 8/83					
155 Human 1700 Randle, Washington 7/94	wamach				
156 Human 8179 Lander, Wyoming 7/93	wyol				
157 Pm 458 Mentone, Loving Co., Texas 3/87	rtx458				
158 Pm 460 Quemado, Catron Co., New Mexico 1/mm460					
159 Pm 433 S. Cle Elum, Kittitas Co., Washington rw4433					
160 Human 0669 Toledo, Washington 6/96	washcc				
161 Pm 206 Lynnwood, Washington 5/96	wash206				
162 Pm 432 S. Cle Elum, Kittitas Co., Washington rw4432					
163 Pm 2257 Middle River Res., Fort St.James Bcncb257					
164 Human 0011Merritt, British Columbia, Canada kamloops					
165 Prg,fasc 727 Moffat, Colorado 6/94	rco727				
166 Human CO H5 Hesperus, Colorado 5/93	pron	L27772	Human 0013 Glenwood Springs, Colorado 7/94	Pm CO R1 Hesperus, Colorado 6/93	Pm CO R2 Grand Junction, Colorado 6/93
167 Human 0013 Glenwood Springs, Colorado 7/94					
168 Pm CO R1 Hesperus, Colorado 6/93					
169 Pm CO R2 Grand Junction, Colorado 6/93					
170 Pm CO R3 Grand Junction, Colorado 7/93	proq	L27775			
171 Pm 440 La Plata, San Juan Co., New Mexico mm440					
172 Human CO H6 Norwood, Colorado 6/93	proo	L27773			
173 P. sp. 462 Cimarron, Montrose Co., Colorado rco462					
174 Human CO H7 Molina, Mesa Co., Colorado 3/5/prop		L27774			
175 Pm 708 NPS4, Kansas 7/94	rks708		Pm 709 NPS4, Kansas 7/94		
176 Pm 709 NPS4, Kansas 7/94					
177 Pm 071 Fort Steele, Carbon Co., Wyoming 7/94					
178 Pm 016 Thermopolis, Hot Springs Co., Wyoming 7/94					
179 Human AZ H18 Fort Defiance, Arizona 7/93	proe	L27763			

180 Pm 459 Quemado, Catron Co., New Mexico 1/mm459				
181 Pm NM R35 Bread Springs, New Mexico 6/93 proj	L27794	L27793		
182 Pm NM R34 Crownpoint, New Mexico 6/93 proj	L27792	L27791	Pm NM R32 Crown Point, New Mexico 6/93	Pm NM R4 Pinehill/Ramah, New Mexico 6/93
183 Pm NM R33 Bread Springs, New Mexico 6/93 proj	L27790		Pm AZ R5 Springerville, Arizona 6/93	Pm AZ R6 Springerville, Arizona 6/93
184 Pm NM R31 Bread Springs, New Mexico 6/93 proj	L27791			
185 Pm NM R32 Bread Springs, New Mexico 6/93 proj	L27792			
186 Pm NM R4 Pinehill/Ramah, New Mexico 6/93	L27793			
187 Pm AZ R5 Springerville, Arizona 6/93	L27794			
188 Pm AZ R6 Springerville, Arizona 6/93	L27795			
189 Human AZ H16 Alpine Ranchero, Arizona 6/93 proj	L27761	L27762	Human 0164 Fort Defiance, Arizona 10/93	
190 Human AZ H17 Indian Wells, Arizona 6/93 proj	L27762	L27760	Pm AZ R7 Black Mesa, Arizona 6/93	
191 Human 0164 Fort Defiance, Arizona 10/93	L27763	L27768		
192 Human AZ H15 St. Michaels, Arizona 7/93 prob	L27760	L27768		
193 Pm AZ R7 Black Mesa, Arizona 6/93	L27768	L27767		
194 Tam quad, AZ R30 Black Mesa, Arizona 6/93 proj	L27767	L25783	Pm NM R11 Pinehill/Ramah, New Mexico 6/93	Pm NM R12 Pinehill/Ramah, New Mexico 6/93
195 Pm 434 Animas Valley, Hidalgo Co., New Mex mm434	L27768	L25783	Pm NM R11 Pinehill/Ramah, New Mexico 6/93	Pm NM R12 Pinehill/Ramah, New Mexico 6/93
196 Pt AZ R29 Black Mesa, Arizona 6/93 proj	L27769	L27770	Pm NM R25 Bread Springs, New Mexico 6/93	
197 Human NM H10 Pinehill/Ramah, New Mexico 6/93msseg	L27770	L27775	Pt NM R13 Pinehill/Ramah, New Mexico 7/proz	
198 Pm NM R11 Pinehill/Ramah, New Mexico 6/93	L27775	L27774	Pt NM R26 Crownpoint, New Mexico 6/93	
199 Pm NM R12 Pinehill/Ramah, Arizona 6/93	L27776	L27778	Tam. dors. NM R22 Bread Springs, New Mexico 6/93	
200 Human AZ H11 Black Mesa, Arizona 6/93 proj	L27778	L27783	Pm NM R8 Pinehill/Ramah, New Mexico 6/93	Pm NM R9 Pinehill/Ramah, New Mexico 6/93
201 Pm NM R24 Bread Springs, New Mexico 6/93 proj	L27779	L27783	Pm NM R9 Pinehill/Ramah, New Mexico 6/93	Pm NM R10 Pinehill/Ramah, New Mexico 6/93
202 Pm NM R25 Bread Springs, New Mexico 6/93	L27780			
203 Pm NM R13 Pinehill/Ramah, New Mexico 6/93projaa	L27785			
204 Human NM H9 Pinehill/Ramah, New Mexico 7/proz	L27784			
205 Pt NM R26 Crownpoint, New Mexico 6/93	L27785			
206 Muus must, NM R23 Fort Wingate, New Mexico/proeae	L27786			
207 Pm NM R21 Bread Springs, New Mexico 6/93 prob	L27787			
208 Tam. dors. NM R22 Bread Springs, New Mexico 6/93	L27788			
209 Human NM H8 Pinehill/Ramah, New Mexico 5/proy	L27789			
210 Pm NM R8 Pinehill/Ramah, New Mexico 6/93	L27790			
211 Pm NM R9 Pinehill/Ramah, New Mexico 6/93	L27791			
212 Pm NM R10 Pinehill/Ramah, New Mexico 6/93	L27792			
213 Pm 463 S.Cuba, Sandoval Co., New Mexico 7/mm463	L27793			
214 Human NM H14 Gallup, New Mexico 7/93	L27794			
215 Pt AZ R20 Black Mesa, Arizona 6/93	L27795			
216 Pt AZ R19 Black Mesa, Arizona 6/93	L27796			
217 Pm AZ R14 Black Mesa, Arizona 6/93	L27797			
218 Human AZ H3 Pinon, Arizona 7/93	L27798			
219 Pm NM R16 Crownpoint, New Mexico 6/93	L27799			
220 Pm NM R17 Crownpoint, New Mexico 6/93	L27799			
221 Human NM H2 Vanderwagon, New Mexico 7/prox	L27799			
222 T.dors. NM R16 Ramah, New Mexico 6/93	L27799			
223 Human NM H1 Church Rock, New Mexico 6/93:prot	L27799			
224 Pm NM R15 Crownpoint, New Mexico 6/93	L27799			
225 Human NM H2 Sedan, New Mexico 4/93	L27799			
226 Human NM H3 Littlewater, New Mexico 6/93	L27799			
227 Pm NM R27 Crownpoint, New Mexico 6/93	L27799			
228 Pm NM R26 Crownpoint, New Mexico 6/93	L27799			
229 Human 0038 Santa Fe, New Mexico 3/94	L27799			
230 Pm 457 Durmas, Moore Co., Texas 9/85	L27799			
231 Human 1001 Holman, Korean 10/93	L27799			
232 Human 8577 Elkhart, Kansas 10/93	L27799			
233 Pi 4787 Oro Grande, Otero Co., Texas 7/93	L27799			
234 Pm 450 Dimmitt, Castro Co., Texas 3/88	L27799			
235 Pm 442 Dimmitt, Castro Co., Texas 3/88	L27799			
236 Pm 443 Dimmitt, Castro Co., Texas 3/88	L27799			
237 Pm 444 Dimmitt, Castro Co., Texas 3/88	L27799			
238 Pm 446 Dimmitt, Castro Co., Texas 3/88	L27799			
239 Pm 447 Dimmitt, Castro Co., Texas 3/88	L27799			
240 Pm 449 Dimmitt, Castro Co., Texas 3/88	L27799			
241 Pm 452 Dimmitt, Castro Co., Texas 5/88	L27799			
242 Pm 453 Dimmitt, Castro Co., Texas 5/88	L27799			
243 Pm 445 Wells, Elko Co., Texas 6/88	L27799			
244 Human CO H4 Sawmill, Arizona 7/93	L27799			
245 Human 1047 Bridgehampton, New York 4/95	L27799			
246 Pi NY-1 Shelter Is., New York 10/94	L27799			
247 Pi NY-2 Shelter Is., New York 10/94	L27799			
248 Human 5800 Shelter Is., New York 1/94	L27799			
249 PJ 085 Rhode Is. 7/94	L27799			
250 PJ 086 Rhode Is. 7/94	L27799			
251 PJ 603 Rhode Is. 7/94	L27799			
252 Pi 605 Rhode Is. 7/94	L27799			
253 Pi 012 Rhode Is. 7/94	L27799			
254 Pi 014 Rhode Is. 7/94	L27799			
255 Pi 083 Rhode Is. 7/94	L27799			
256 Pm 2255 Mont Tremblant Park, Quebec, Cana cnqb2255	L27799			
257 Pm 305 E. Algonquin Park, Ontario, Canada farcn305	L27799			
258 Pm 306 E. Algonquin Park, Ontario, Canada farcn306	L27799			
259 Pm 32 Madison Co., Virginia 6/94	L27799			
260 Pm 322 Madison Co., Virginia 6/94	L27799			
261 Pm 323 Madison Co., Virginia 6/94	L27799			
262 Pm 320 Madison Co., Virginia 6/94	L27799			
263 Pm 80 Madison Co., Virginia 6/94	L27799			
264 Pi 319 Rappahannock Co., Virginia 6/94	L27799			
265 Pm 314 Cambria Co., Pennsyl. 7/94	L27799			
266 Pm 315 Cambria Co., Pennsyl. 7/94	L27799			
267 Pi 313 Cambria Co., Pennsyl. 7/94	L27799			
268 Pm 441 Rector, Westmoreland Co., Pennsyl. 1/pa441	L27799			
269 Monongahela-2 Bolair, Webster Co., West Virghmu32653	L27799			

270 Pm 2158 Timmins, Ontario, Canada 8/95 cnon2158

271 Pm 2220 Timmins, Ontario, Canada 8/95

272 Pm 2629 Gagetown, New Brunswick, Canada cnvb229

273 Pm 2256 Saguenay, Quebec, Canada 9/95 cnvb226

274 Pm 1083 Baie-Comeau, Quebec, Canada 16cmvb203

275 Pm 2248 Baie-Gaspé, Quebec, Canada 8/95cb227

276 Pm 2227 RnV Gaspé Penn., Quebec, Canada cnvb227

277 Human 0027 Tuckasegee, N. Carolina 9/95 smch1

278 Pm 317 Sevier Co., Tennessee 6/94 rnr317

279 Pi 707 Chickasaw, Murray Co., Oklahoma 7/94rk707

280 Pi 9436372 Westville, LaPorte Co., Indiana 8/rind4

281 Pi 9436368 Westville, LaPorte Co., Indiana 7/94

282 Pi 9436245 Westville, LaPorte Co., Indiana 7/94

283 Pi 9436244 Westville, LaPorte Co., Indiana 7/94

284 Pi 9436378 Westville, LaPorte Co., Indiana 8/rin378

285 Pi 170 Thousand Hills St. Park, Adair Co., Missouri 12/94

286 Pi 189 Thousand Hills St. Park, Adair Co., Missouri 2/94

287 Pi 195 Thousand Hills St. Park, Adair Co., Missouri 2/94

288 Pi 212 Thousand Hills St. Park, Adair Co., Missouri 2/94

Pm 2220 Timmins, Ontario, Canada 8/95

Pi 9436368 Westville, LaPorte Co., Indiana 7/94

Pi 9436245 Westville, LaPorte Co., Indiana 7/94

Pi 9436244 Westville, LaPorte Co., Indiana 7/94

Pi 189 Thousand Hills St. Park, Adair Co., Missouri 2/94

Pi 195 Thousand Hills St. Park, Adair Co., Missouri 2/94

Pi 212 Thousand Hills St. Park, Adair Co., Missouri 2/94

#NEXUS

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phu33256 CAGAGAATGT TAGCAACAAA GGATTCA TTT CAGTCATT CA ATATCACAGA
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phu33251 CAAAGAATGC TGGCAACAAA GGATTCTTT CAATCATT CA ATATCACTGA
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rva319 CGGAGGATGA TGGCCACAAAG AGATTCA TTT CAGTCATT CA ATGTATCAGA
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hpsmseg	CAACGCATGA	TGGCAACTCG	AGATTCTTTC	CAGTCATTCA	ATGTGACAGA
proa	CAACGCATGA	TGGCAACTCG	AGATTCTTTC	CAGTCATTCA	ATGTGACAGA
proaf	CAACGCATGA	TGGCAACTCG	AGATTCTTTC	CAGTCATTCA	ATGTGACAGA
proaa	CAACGCATGA	TGGCAACTCG	AGATTCTTTC	CAGTCATTCA	ATGTGACAGA
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proaj	CAACGCATGA	TGGCAACTCG	AGATTCTTC	CAGTCATTCA	ATGTGACAGA
proah	CAACGCATGA	TGGCAACTCG	AGATTCTTC	CAATCATTCA	ATGTGACAGA
proag	CAACGCATGA	TGGCAACTCG	AGATTCTTC	CAATCATTCA	ATGTGACAGA
proc	CAGCGCATGA	TGGCAACTCG	AGATTCTTC	CAATCATTCA	ATGTGACAGA
rnm459	CAACGCATGA	TGGCAACTCG	AGATTCTTC	CAATCATTCA	ATGTGACAGA
prod	CAACGCATGA	TGGCAACTCG	AGATTCTTC	CAATCATTCA	ATGTGACAGA
proai	CAACGCATGA	TGGCAACTCG	AGATTCTTC	CAATCATTCA	ATGTGACAGA
proae	CAACACATGA	TGGCAACTCG	AGATTCTTC	CAGTCATTCA	ATGTGACAGA
pread	CAACGCATGA	TGGCAACTCG	AGATTCTTC	CAGTCATTCA	ATGTGACAGA
prob	CAGCGCATGA	TGGCAACTCG	AGATTCTTC	CAATCATTCA	ATGTGACAGA
proj	CAGCGCATGA	TGGCAACTCG	AGATTCTTC	CAATCATTCA	ATGTGACAGA
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prow	CAGCGCATGA	TGGCAACTAG	AGATTCTTC	CAATCATTCA	ATGTGACAGA
prov	CAGCGCATGA	TGGCAACTAG	AGATTCTTC	CAATCATTCA	ATGTGACAGA
ks2	CAGCGCATGA	TGGCAACTAG	AGATTCTTC	CAATCATTCA	ATGTAACAGA
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rco727	CAGCGCATGA	TGGCAACCCG	AGATTCTTC	CAATCATTCA	ATGTTACAGA
pron	CAGCGCATGA	TGGCAACTCG	AGATTCTTC	CAATCATTCA	ATGTTACAGA
rks708	CAGCGCATGA	TGGCAACTCG	AGATTCTTC	CAATCATTCA	ATGTGACAGA
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prom	CAGCGCATGA	TGGCAACTAG	AGATTCTTT	CAGTCATTCA	ATGTAACAGA
proh	CAGCGCATGA	TGGCAACTAG	AGATTCTTT	CAATCATTCA	ATGTAACAGA
prog	CAGCGCATGA	TGGCAACTAG	AGATTCTTT	CAATCATTCA	ATGTAACAGA
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rwa432	CAGCGCATGA	TGGCAACTCG	GGATTCTTC	CAGTCATTCA	ATGTGACAGA
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kamloops	CAACGCATGA	TGGCAACTCG	AGATTCTTT	CAATCATTCA	ATGTGACAGA
9608868m	CAGCGTATGA	TGGCTACACG	GGATTCTTT	CAATCATTCA	ATGTGACAGA
ind	CAACGTATGA	TGGCTACACG	AGATTCTTT	CAATCGTTCA	ACGTGACAGA
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rind4	AAGAGGATGA	TGGCCACGAG	GGATTCTTTT	CAATCATTAA	ATGTGACAGA
rin378	AAGAGGATGA	TGGCCACGAG	GGATTCTTTT	CAATCATTAA	ATGTGACAGA
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vn757	AAAAGATTGA	TGGCAACTAA	AGACTCATTT	CAGTCATTAA	ATGTTCCGA
hvimsega	AAAAGATTGA	TGGCTACAAA	GGACTCGTTT	CAGTCATTAA	ATGTATCTGA
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pvu22418	AAAAGAATGA	TTGCAACAAA	GGATTCTTT	CAATCATTCA	ATGTTACAGA
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puumseg	AAGAGGATGA	TTGCCACAAA	GGATTCTTT	CAATCTTTCA	ATGTGACAGA
puvmvin83	AAACGGATGA	TTGCTACTAA	AGATTCTTC	CAGTCCTTTA	ATGTTACAGA
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hnvdobms	AAGAAAGTAA	TGGCAACTAT	TGATTCTTT	CAGTCATTAA	ACACTAGCTC
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htnlee	AAGAAAGTAA	TGGCAACAAAT	TGATTCTTT	CAATCTTTA	ATACAAGCAC
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seo8039	AAGAAAGTTC	TTGCAACAAAT	TGATTCTTC	CAATCATTAA	ACACAAGCAA
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[51

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mf113	ACCACATATC	ACAGCTAACT	CACTAGAATG	GGTTGATCCT	GATAGTTCAT
khu35254	accacatatac	acagctaatt	cactagaatg	ggtttagtcc	gatagttcat
tulmmor93	ACCTCATATT	ACAAACAAAAT	CACTAGAATG	GGTTGACCCA	GATAGTTCTC
tulvm86m	ACCTCATATT	ACAACAAATT	CACTAGAATG	GGTTGACCCA	GATAGTTCTC
tulmt249	ACCCCATATC	ACAACAACT	CTCTAGAGTG	GTTAGATCCT	GATAGTTCAC
tulmt53m	ACCCCACATT	ACAACAAATT	CTCTAGAATG	GTTAGATCCT	GATAGTTCAT
phvmsrna	ACCACATATT	ACCAGCAATT	CACTTGAATG	GTTAGATCCA	GATAGTTCAT
phu33240	ACCACATATC	ACCGTAACT	CACTTGAGTG	GGTTGATCCA	GATAGTTCTC
mm3485wy	ACCACATATA	ACTAGTAACT	CACTTGAGTG	GGTTGATCCA	GATAGCTCTT
phu33256	GCCACACATA	ACCGTAATT	CACTTGAGTG	GGTTGATCCT	GATAGTTCTC
phu33254	GCCACACATT	ACCGTAATT	CATTGGAGTG	GGTTGATCCA	GATAGCTCCT
phu33251	ACCACATATT	ACCGCAATT	CATTGGAGTG	GGTTGATCCA	GATAGCTCTT
phu33247	ACCACATATT	ACCGCAATT	CATTAGAGTG	GGTTGATCCA	GATAGCTCTC
phu33245	ACCACATATT	ACCGCAATT	CATTGGAGTG	GGTTGATCCA	GATAGCTCTC
pm1047oh	ACCACATATC	ACCGTAATT	CTTTAGAATG	GTTGGATCCA	GATAGTTCTT
r1051oh	ACCACATATC	ACCGTAATT	CTTTAGAATG	GTTAGATCCA	GATAGTTCTT
r1049oh	ACCACATATC	ACCGTAATT	CTTTAGAATG	GTTAGATCCA	GATAGTTCTT
cnqb2255	ACCGCATATC	ACTAACAAAC	GTCTTGAGTG	GATTGATCCT	GATAGCAGTA
rva319	ACCGCATATT	ACCAAGAAC	GTCTTGAGTG	GATTGATCCT	GATAGCAGTA
hmu32653	accacatatt	accagcaacc	gtcttgagtg	gattgatcct	gatagcagta
rpa441	ACCGCATATC	ACCAAGAAC	GTCTTGAGTG	GATTGATCCT	GATAGCAGTA
rpa313	ACCGCATATC	ACCAAGAAC	GTCTTGAGTG	GATTGATCCT	GATAGCAGTA
rpa31415	ACCGCATATC	ACCAAGAAC	GTCTTGAGTG	GATTGATCCT	GATAGCAGTA
rcn306	GCCACATATT	ACCAAGAAC	GTCTTGAGTG	GATTGATCCT	GACAGCAGTA
rcn305	GCCACATATT	ACCAAGAAC	GTCTTGAGTG	GATTGATCCT	GACAGCAGTA
rva321	ACACATATC	ACCAAGAAC	GTCTTGAGTG	GATTGATCCT	GACAGCAGTA
rva32223	ACACATATC	ACCAAGAAC	GTCTTGAGTG	GATTGATCCT	GACAGCAGTA
rva320	ACACATATC	ACCAAGAAC	GTCTTGAGTG	GACTGATCCT	GACAGCAGTA
va803	ACACATATC	ACCAAGAAC	GTCTTGAGTG	GACTGATCCT	GACAGCAGTA
cnon2158	GCCACATATT	ACTAGTAATC	GTCTTGAGTG	GATTGATCCT	GATAGTAGTA
cnnb2629	GCCACATATC	ACTAGTAATC	GACTCGAGTG	GATTGATCCA	GATAGTAGCA
cnqb2256	GCCACATATC	ACTAGTAACC	GACTTGAGTG	GATTGATCCT	GATAGTAGCA
cnnb2083	GCCACATATC	ACTAGTAACC	GGCTTGAGTG	GATTGATCCT	GATAGTAGCA
cnqb2237	GCCACATATC	ACTAGCAACC	GGCTTGAGTG	GATTGATCCT	GATAGTAGTA
cnqb2227	GCCACATATC	ACTAGCAACC	GGCTTGAGTG	GATTGATCCT	GATAGTAGTA

hny131	ACCACACATC	ACCGAGCAATC	GCCTTGAAATG	GATTGATCCT	GATAGCAGTA
nyu36802	ACCGCACATT	ACCGAGCAATC	GTCTTGAAATG	GATTGATCCT	GATAGCAGTA
nyu36803	ACCGCACATT	ACCGAGTAATC	GTCTTGAAATG	GATTGATCCT	GATAGCAGTA
nyu36801	ACCGCACATT	ACCGAGTAATC	GCCTTGAAATG	GATTGATCCT	GATAGCAGTA
rrigrp2	ACCACACATT	ACTAGTAACC	GTCTTGAGTG	GATTGATCCT	GATAGTAGTA
rrigrp1	ACCACACATT	ACTAGTAACC	GTCTTGAGTG	GATTGATCCT	GATAGTAGTA
snnchl	CCCCCATATA	ACTAGCAATC	GCCTTGAAATG	GATTGACCCA	GATAGTAGTA
rtn317	GCCCCACATA	ACTAGTAATC	GTCTTGAAATG	GATTGATCCG	GATAGCAGCA
id8673	ACCGCACATT	ACTAGTAACC	GACTTGAGTG	GATTGATCCA	GACAGTAGTA
rcn332	ACCACACATT	ACTAGTAATC	GGCTTGAAATG	GATTGATCCA	GACAGTAGTA
mt2978	ACCTCACATA	ACTAGTAATC	GGCTTGAAATG	GATTGATCCG	GACAGTAGTA
pror	ACCTCATATA	ACTAGTAATC	GGCTTGAAATG	GATTGATCCA	GACAGTAGTA
snu33238	GCCACATATT	ACCGAGCAATC	GACTTGAAATG	GATTGATCCA	GATAGTAGTA
id6007	ACACATATT	ACCGAGTAATC	GACTTGAAATG	GATTGATCCA	GATAGTAGTA
ror428	ACACACATT	ACCGAGCAATC	GACTTGAAATG	GATTGATCCA	GATAGTAGTA
rut313	ACACATATT	ACCGAGCAACC	GACTTGAAATG	GATTGATCCA	GATAGTAGTA
snu33239	ACACATATT	ACCGAGCAATC	GACTTGAAATG	GATTGATCCA	GATAGTAGTA
nvr233	ACACATATT	ACCGAGCAATC	GACTTGAAATG	GATTGATCCA	GATAGTAGTA
hvu44992	ACACATATT	ACCGAGCAATC	GACTTGAAATG	GATTGATCCA	GATAGTAGTA
snu33229	ACACATATT	ACCGAGCAATC	GACTTGAAATG	GATTGATCCA	GATAGTAGTA
rut315	GCCACATATT	ACCGAGCAATC	GACTTGAATG	GATTGATCCA	GATAGTAGTA
snu33227	ACACATATT	ACCGAGCAATC	GACTTGAATG	GATTGATCCA	GATAGTAGTA
prol	ACACATATT	ACCGAGCAATC	GACTTGAATG	GATTGATCCA	GATAGTAGTA
rut309	ACACATATT	ACCGAGCAATC	GACTTGAATG	GATTGATCCA	GACAGTAGTA
hvu44991	ACACATATT	ACCGAGCAATC	GACTTGAATG	GATTGATCCA	GACAGTAGTA
snu33445	GCCACACATC	ACCAAGTAATC	GACTTGAGTG	GATTGATCCA	GATAGTAGTA
proak	ACACACATT	ACCAAGCAATC	GACTTGAGTG	GATTGACCCA	GATAGTAGTA
snu33257	ACACACATT	ACCAAGCAATC	GACTTGAGTG	GATTGATCCA	GATAGTAGTA
snu33223	ACACACATT	ACTAGCAATC	GACTTGAGTG	GATTGATCCA	GATAGTAGTA
snu33221	ACACACATT	ACTAGCAATC	GACTTGAGTG	GATTGATCCA	GACAGTAGTA
snu33224	ACACACATT	ACTAGCAATC	GACTTGAGTG	GATTGATCCA	GATAGTAGTA
snu33219	ACACACATT	ACTAGCAATC	GACTTGAGTG	GATTGATCCA	GATAGTAGTA
snu33222	ACACACATT	ACCAAGCAATC	GACTTGAGTG	GATTGATCCA	GATAGTAGTA
snu33262	ACACACATT	ACCAAGCAATC	GACTTGAGTG	GATTGATCCA	GATAGTAGTA
rtx458	ACACATATC	ACTAGTAACC	GACTTGAGTG	GATTGATCCA	GATAGTAGTA
rnm460	ACACATATC	ACTAGTAACC	GACTTGAGTG	GATTGATCCA	GATAGCAGTA
proe	ACACACATC	ACTAGCAACC	GCCTTGAGTG	GATTGATCCA	GATAGCAGTA
proy	ACACATATC	ACTAGCAACC	GACTTGAGTG	GATTGATCCA	GATAGTAGTA
hpsmseg	ACACATATC	ACTAGCAACC	GACTTGAGTG	GATTGATCCA	GATAGCAGTA
proa	ACACATATC	ACTAGCAACC	GACTTGAGTG	GATTGATCCA	GATAGCAGTA
proaf	ACACATATC	ACTAGCAACC	GACTTGAGTG	GATTGATCCA	GATAGCAGTA
proaa	ACACATATC	ACTAGCAACC	GACTTGAGTG	GATTGATCCA	GATAGCAGTA
proz	ACACATATC	ACTAGCAACC	GACTTGAGTG	GATTGATCCA	GATAGCAGTA
proaj	ACCGCATATT	ACTAGCAACC	GACTTGAGTG	GATTGATCCA	GATAGCAGTA
proah	ACACATATT	ACTAGCAACC	GACTTGAGTG	GATTGATCCA	GATAGCAGTA
proag	ACACATATT	ACTAGCAACC	GACTTGAGTG	GATTGATCCA	GATAGCAGTA
proc	ACACATATT	ACTAGCAACC	GACTTGAGTG	GATTGATCCA	GATAGCAGTA
rnm459	ACACATATC	ACTAGCAACC	GGCTTGAGTG	GATTGATCCA	GATAGCAGTA
prod	ACACATATC	ACTAGCAACC	GACTTGAGTG	GATTGATCCA	GATAGCAGTA
proai	ACCGCATATC	ACTAGCAACC	GACTTGAGTG	GATTGATCCA	GATAGCAGTA
proae	ACACATATC	ACTAGCAACC	GACTTGAGTG	GATTGATCCA	GATAGCAGTA
proad	ACACATATC	ACTAGCAACC	GACTTGAGTG	GATTGATCCA	GATAGCAGTA
prob	ACACATATC	ACTAGCAACC	GACTTGAGTG	GATTGATCCA	GATAGCAGTA
proj	ACACATATC	ACTAGCAACC	GACTTGAGTG	GATTGATCCA	GATAGCAGTA
rnm434	ACACATATC	ACTAGCAACC	GACTTGAGTG	GATTGATCCA	GATAGCAGTA
roi	ACACATATC	ACTAGCAACC	GACTTGAGTG	GATTGATCCA	GATAGCAGTA
rnm463	ACACATATC	ACTAGCAACC	GACTTGAGTG	GATCGATCCA	GATAGTAGTA
rtx457	ACACATATC	ACGAGCAACC	GGCTTGAGTG	GATTGATCCA	GATAGTAGTA
pl4787	ACACATATC	ACTAGCAACC	GACTTGAGTG	GATTGATCCA	GATAGTAGTA
rtx450	ACACATATC	ACTAGCAACC	GACTTGAGTG	GATTGATCCA	GATAGTAGTA
rtx1	ACACATATC	ACTAGCAACC	GACTTGAGTG	GATTGATCCA	GATAGTAGTA
rtx445	ACACATATC	ACTAGCAACC	GACTTGAGTG	GATTGATCCA	GATAGTAGTA
prow	ACACATATT	ACTAGCAACC	GACTTGAGTG	GATTGATCCA	GATAGTAGTA
prov	ACACATATC	ACTAGCAACC	GACTTGAGTG	GATTGATCCA	GATAGTAGTA
ks2	ACACATATC	ACTAGCAACC	GACTTGAGTG	GATTGATCCA	GATAGTAGTA
kansas	ACACATATC	ACTAGCAACC	GACTTGAGTG	GATTGATCCA	GATAGTAGTA
rco727	ACACATATC	ACTAGTAACC	GACTCGAATG	GATTGATCCA	GATAGTAGTA
pron	ACACATATC	ACTAGTAACC	GACTTGAGTG	GATTGATCCA	GATAGTAGTA
rks708	ACACACATC	ACCAAGTAACC	GACTTGAGTG	GATTGATCCA	GATAGTAGTA
wy29071	ACACACATC	ACTAGTAACC	GACTTGAGTG	GATTGATCCA	GATAGTAGTA
wy29016	ACACACATC	ACTAGTAACC	GACTTGAGTG	GATTGATCCA	GATAGTAGTA
prog	ACACATATC	ACTAGTAACC	GACTTGAGTG	GATTGATCCA	GATAGTAGTA
rco462	ACACACATC	ACTAGTAACC	GACTTGAGTG	GATTGATCCG	GATAGTAGTA
prop	ACACATATC	ACTAGTAACC	GACTTGAGTG	GATTGATCCG	GATAGTAGTA
rnm440	ACACATATC	ACTAGTAACC	GTCTTGAGTG	GATTGATCCA	GATAGTAGTA
proo	ACACATATC	ACTAGTAACC	GTCTTGAGTG	GATTGATCCA	GATAGTAGTA
prom	ACACACATT	ACTAGCAACC	GGCTTGAGTG	GATTGATCCA	GATAGTAGTA
proh	ACACACATT	ACTAGCAACC	GACTTGAGTG	GATCGATCCA	GATAGTAGTA
prog	ACACACATT	ACTAGCAACC	GACTTGAGTG	GATTGATCCA	GATAGTAGTA
prof	ACACACATT	ACTAGCAACC	GACTTGAGTG	GATTGATCCA	GATAGTAGTA
proac	GCCACACATC	ACTAGCAACC	GACTTGAGTG	GATTGATCCA	GATAGTAGTA

proab	GCCACACATC	ACTAGCAACC	GACTTGAGTG	GATTGATCCA	GATAGTAGCA
prot	GCCACACATT	ACTAGCAACC	GACTTGAGTG	GATTGATCCA	GATAGTAGCA
prox	GCCACACATT	ACTAGCAACC	GACTTGAGTG	GATTGATCCA	GATAGTAGCA
az9360	ACCACACATT	ACTAGTAATC	GACTTGAGTG	GATTGATCCA	GATAGTAGTA
wy29054	ACCACATATT	ACAAGTAATC	GACTTGAGTG	GATTGATCCT	GATAGTAGTA
ut0009	GCCACACATT	ACTAGTAACC	GCCTTGAGTG	GATTGATCCT	GACAGTAGTA
snu33233	GCCACACATT	ACTAGTAACA	GACTTGAGTG	GATTGATCCT	GACAGTAGTA
nvr0609	GCCACACATT	ACTAGTAACC	GACTTGAGTG	GATTGACCT	GACAGTAGTA
snu33236	GCCACACATT	ACTAGTAACC	GACTAGAGTG	GATTGATCCT	GACAGTAGTA
snu33231	GCCACACATT	ACTAGTAACC	GACTTGAGTG	GATTGATCCT	GACAGTAGTA
snu33234	GCCACACATT	ACTAGTAACC	GACTTGAGTG	GATTGATCCT	GACAGTAGTA
snu33244	GCCACACATT	ACTAGTAACC	GACTTGAGTG	GATTGATCCT	GACAGTAGTA
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snu33264	GCCACACATT	ACTAGTAACC	GACTTGAAATG	GATTGATCCT	GACAGTAGTA
prok	GCCACACATC	ACTAGTAACC	GACTTGAGTG	GATTGATCCT	GACAGTAGTA
wamach	GCCACATATT	ACTAGTAACC	GACTTGAGTG	GATTGATCCT	GATAGTAGTA
wyol	ACCACATATT	ACTAGTAACC	GACTTGAGTG	GATTGATCCT	GATAGTAGTA
yukon	GCCCCACATT	ACTAGTAATC	GACTTGAATG	GATTGATCCA	GATAGTAGCA
rcn329	GCCTCACATT	ACTAGTAATC	GACTTGAATG	GATTGATCCA	GATAGTAGCA
wy28992	GCCTCATATT	ACTAGTAATC	GACTTGAGTG	GATTGATCCA	GATAGTAGCA
rcn333	GCCTCATATT	ACTAGTAATC	GACTTGAGTG	GATTGATCCA	GATAGTAGCA
hcn039	GCCTCATATT	ACTAGTAATC	GACTTGAGTG	GATTGATCCA	GATAGTAGCA
rcn330	GCCTCATATT	ACTAGTAATC	GACTTGAGTG	GATTGATCCA	GATAGTAGCA
ndr761	ACCTCATATT	ACTAGTAATC	GACTTGAGTG	GATTGATCCA	GACAGTAGCA
rwa433	GCCACACATC	ACAAGTAATC	GGCTTGAGTG	GATTGATCCA	GATAGTAGTA
washcc	ACCACACATC	ACAAGTAATC	GACTAGAGTG	GATTGATCCA	GATAGTAGTA
washr206	ACCACACATC	ACAAGTAATC	GACTAGAGTG	GATTGATCCA	GATAGTAGTA
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cdbc2257	ACCACACATC	ACAAGCAACC	GGCTTGAATG	GATTGATCCA	GATAGTAGTA
kamloops	ACCACACATC	ACAAGTAACC	GGCTTGAATG	GATTGATCCA	GATAGTAGTA
9608868m	GCCTCATATT	ACTAGTAATC	GACTTGAGTG	GATTGATCCA	GATAGTAGTA
ind	GCCTCATATT	ACTAGTAATC	GACTTGAGTG	GATTGATCCT	GATAGTAGTA
ndr793	GCCTCATATC	ACAAGCAACC	GACTTGAATG	GATTGATCCA	GATAGTAGTA
wy28923	GCCTCATATC	ACGAGCAATC	GACTTGAGTG	GATTGATCCA	GATAGTAGTA
ndr805	GCCTCATATT	ACAAGCAATC	GACTTGAGTG	GATTGATCCA	GATAGTAGTA
pros	GCCTCATATC	ACGAGCAATC	GACTTGAGTG	GATTGATCCA	GATAGTAGTA
rok707	ACCTCATATA	ACTAGTAACC	GACTAGAATG	GATTGACCT	GACAGTAGTA
mo1234	ACCTCATATA	ACTAGTAATA	GACTGGAATG	GATTGATCCT	GACAGTAGCA
rind4	ACCGCATATC	ACCAAGTAACC	GATTAGAATG	GATTGACCT	GACAGTAGTA
rin378	ACCGCATATC	ACCAAGTAACC	GATTAGAATG	GATTGACCT	GACAGTAGTA
emu26828	ACCGCACTTA	ACAGCCAATC	TACTGGAATG	GGTGGACCCA	GATAGTACCA
emu33225	ACCACATTTG	ACACAAAATA	TTCTAGAGTG	GGTAGATCCT	GACAGTACCA
emu33260	ACCACATATG	ACACAAAACA	TTCTAGAGTG	GGTAGATCCT	GACAGTACCA
vn757	GGTACATGTC	ACATCAAGCC	AACTTGAATG	GATTGATCCA	GACAGTCAA
hvimsega	AGTACACATT	ACAACAACCA	AGCTAGAATG	GAGTGATCCT	GATAGTAACA
f16169	AGTACACATT	ACAACAAATA	AGTTAGAATG	GAGTGATCCT	GATAGTAACA
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f1210	AGTACACATT	ACAACAAATA	AGCTAGAATG	GAGTGATCCT	GATAGTAACA
f1180	AGTACACATT	ACAACAAATA	AGCTAGAATG	GAGTGATCCT	GATAGTAACA
sc3170	GGCACACATA	ACTACAAACA	GTCTAGAGTG	GATAGACCCA	GACAATAACA
rga4950	GGCACATATA	ACACAAACA	GTCTAGAATG	GATAGATCCA	GACAATAACA
rla268	GGCACATATA	ACACAAACA	GTCTAGAGTG	GGTGGATCCA	GACAATAACA
hviglypre	GGCACACATA	ACACAAACA	GTCTAGAGTG	GGTAGATCCA	GACAATAACA
brazil	TCCACATATA	ACAAACTAAC	AATTAGAATG	GATAGATCCT	GATGGAATA
b9618005	ACCTCATATC	ACAACCAATA	AGCTTGAATG	GATCGATCCA	GATGGAATA
andes	ACCTCACATC	ACAACAAATA	AGCTTGAATG	GATTGACCC	GATGGAATA
b9618007	TCCCCACATC	ACAACAAATA	AACTTGAATG	GATTGACCC	GATGCAACA
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pgh9128	TCCACACATA	ACATCAAGTA	AATTGGAATG	GATAGACCCA	GATGGAATA
pgr8480	TCCACATATA	ACATCAAGTA	AATTGGAATG	GATAGACCCA	GATGGAATA
pgr8434	TCCACACATA	ACATCAAGTA	AATTGGAATG	GATAGATCCA	GATGGAATA
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puumgp	ACCACACATC	TCTACAAGTG	CATTGGAGTG	GATTGACCTA	GATAGTTCAC
puugp2m	ACCTCATATC	TCTGCAAGTT	CACTTGAATG	GATTGATCCT	GATAGTTCTC
pvu22418	ACCCCATATT	TCTGCAAGCT	CACTTGAATG	GATTGACCT	GATAGTTCTT
puuudm	ACCCACATA	TCTGCAAGTG	CATTAGAATG	GATCGATCCT	GACAGTTCAC
puumseg	ACCCCATATT	TCTACAAGTG	CACTTGAATG	GATTGATCCT	GACAGCTCAC
puvmvn83	ACCTCATATC	TCTACAAGTG	CACTCGAATG	GATTGATCAA	GATAGTTCTC
vranicam	ACCCCATATT	TCTACAAGTG	CACTTGAATG	GATTGATCCG	GATAGTTCTC
thai	CATTCACTTT	ACAGATGAAA	GATT...GAT	GGAAGACCC	GATGGCATGT
hnvdobms	AATTCACTAC	ACAGATGAAA	GGATTGAACG	GAAGGACCC	GATGGGATGC
htnhv114	TATGCACTTC	ACTGATGAGA	GAATAGAATG	AAAAGACCC	GATGGAATGT
htnlee	TATGCACTTT	ACTGATGAAA	GGATAGAGTG	AAAAGACCC	GATGGAATGC
hanm	TATGCACTTC	ACTGATGAAA	GGATAGAGTG	AAAAGACCC	GATGGAATGC
seob1	CATACACTTC	ACTGATGAGA	GAATTGAATG	GAGAGACCC	GATGGTATGC
seor11	TATACACTTC	ACTGATGAGA	GAATTGAATG	GAGAGACCC	GATGGCATGC
seo8039	TATACACTTC	ACTGATGAGA	GAATTGAATG	GAGAGACCC	GATGGTATGC
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 snu33262 TTAAAGACCA TATCAACATG GTTCTAAATA GAGATGTTT
 rtx458 TTAAAGATCA CATTAATATG GTTTAAATC GGGATGTTT
 rnm460 TTAAAGATCA TATAAATATG GTTTAAACC GGGATGTTT
 proe TCAAAGATCA TATAAATATG GTTTAAATC GGGATGTTT
 proy TCAAAGATCA TATAAATATG GTTTAAATC GGGATGTTT
 hpsmseg TCAAAGATCA CATTAATATG GTTTAAATC GAGATGTTT
 proa TCAAAGATCA CATTAATATG GTTTAAATC GGGATGTTT
 proaf TCAAAGATCA CATTAACATG GTTTAAATC GGGATGTTT
 proaa TCAAAGATCA CATTAATATG GTTTAAATC GGGATGTTT
 proz TCAAAGATCA CATTAATATG GTTTAAATC GGGATGTTT
 proaj TCAAAGATCA TATAAATATG GTTTAAATC GGGATGTTT

proah	TCAAAGATCA	TATCAATATG	GTTTTAAATC	GGGATGTTT
proag	TCAAAGATCA	TATTAATATG	GTTTTAAATC	GGGATGTTT
proc	TCAAAGATCA	TATTAATATG	GTTTTAAATC	GGGATGTTT
rnm459	TCAAAGATCA	TATTAATATG	GTTTTAAATC	GGGATGTTT
prod	TCAAAGATCA	TATTAATATG	GTTTTAAATC	GGGATGTTT
proai	TCAAAGATCA	TATTAATATG	GTTTTAAATC	GGGATGTTT
proae	TCAAAGATCA	TATTAATATG	GTTTTAAATC	GGGATGTTT
proad	TCAAAGATCA	TATTAATATG	GTTTTAAATC	GGGATGTTT
prob	TCAAAGATCA	TATTAATATG	GTTTTAAATC	GGGATGTTT
proj	TCAAAGATCA	TATTAATATG	GTTTTAAATC	GGGATGTTT
rnm434	TCAAAGATCA	TATTAATATG	GTTTTAAATC	GGGATGTTT
proi	TCAAAGATCA	TATTAATATG	GTTTTAAATC	GGGATGTTT
rnm463	TCAAAGATCA	TATTAATATG	GTTTTAAATC	GGGACGTCT
rtx457	TCAAAGATCA	TATTAATATG	GTGTTAAATC	GGGATGTTT
pl4787	TCAAAGATCA	TATTAATATG	GTTTTAAACC	GAGATGTTT
rtx450	TCAAAGATCA	TATCAATATG	GTTTTAAATC	GAGATGTTT
rtx1	TCAAAGATCA	TATCAATATG	GTTTTAAATC	GAGATGTTT
rtx445	TCAAAGATCA	TATCAATATG	GTTTTAAATC	GAGATGTTT
prow	TCAAAGATCA	TATTAATATG	GTTTTAAATC	GGGATGTTT
prov	TCAAAGATCA	TATTAATATG	GTTTTAAATC	GGGATGTTT
ks2	TCAAAGATCA	TATTAATATG	GTTTTAAATC	GGGATGTTT
kansas	TCAAAGATCA	TATTAATATG	GTTTTAAATC	GGGATGTTT
rco727	TCAAAGACCA	TATTAATATG	GTTTTAAATC	GGGATGTTT
pron	TCAAAGACCA	TATTAATATG	GTTTTAAATC	GGGATGTTT
rks708	TCAAAGATCA	TATTAACATG	GTTTTAAATC	GGGATGTTT
wy29071	TCAAAGATCA	TATTAATATG	GTTTTAAATC	GGGATGTTT
wy29016	TCAAAGATCA	TATTAATATG	GTTTTAAATC	GGGATGTTT
proq	TCAAGGATCA	TATTAATATG	GTTTTAAACC	GGGATGTTT
rco462	TCAAGGATCA	TATTAATATG	GTTTTAAATC	GGGATGTTT
prop	TCAAGGATCA	TATTAATATG	GTTTTAAATC	GGGATGTTT
rnm440	TCAAGGATCA	TATTAATATG	GTTTTAAACC	GGGATGTTT
proo	TCAAGGATCA	TATTAATATG	GTTTTAAATC	GGGATGTTT
prom	TCAAAAGATCA	TATTAATATG	GTTTTAAATC	GAGATGTGT
proh	TCAAAAGATCA	TATTAATATG	GTTTTAAATC	GGGATGTGT
prog	TCAAAAGATCA	TATTAATATG	GTTTTAAATC	GGGATGTGT
prof	TCAAAAGATCA	TATTAATATG	GTTTTAAATC	GGGATGTAT
proac	TCAAAAGATCA	TATTAATATG	ATTTTAAATC	GGGATGTTT
proab	TCAAAAGATCA	TATTAATATG	GTTTTAAATC	GGGATGTTT
prot	TCAAAAGATCA	TATTAATATG	GTTTTAAATC	GGGATGTGT
prox	TCAAAAGATCA	TATTAATATG	GTTTTAAATC	GGGATGTTT
az9360	TCAAAGACCA	TATTAATATG	GTTTTAAATC	GAGATGTTT
wy29054	TCAAAGACCA	TATTAATATG	GTTTTAAATC	GGGATGTTT
ut0009	TCAAAGACCA	TATTAATATG	GTTTTAAATC	GGGATGTTT
snu33233	TTAAAGACCA	TATTAATATG	GTTTTAAATC	GGGATGTTT
nvr0609	TCAAAGACCA	TATTAATATG	GTTTTAAATC	GGGATGTTT
snu33236	TCAAAGACCA	TATTAATATG	GTTTTAAATC	GGGATGTTT
snu33231	TCAAAGACCA	TATTAATATG	GTTTTAAATC	GGGATGTTT
snu33234	TCAAAGACCA	TATTAATATG	GTTTTAAATC	GGGATGTTT
snu33244	TCAAAGACCA	TATTAATATG	GTTTTAAATC	GGGATGTTT
snu33230	TCAAAGACCA	TATTAATATG	GTTTTAAATC	GGGATGTTT
snu33264	TCAAAGACCA	TATTAATATG	GTTTTAAATC	GGGATGTTT
prok	TCAAAGACCA	TATTAATATG	GTTTTAAATC	GGGATGTTT
wamach	TCAAGGATCA	TATTAATATG	GTTTTAAATC	GGGATGTTT
wyol	TTAAAGATCA	TATTAATATG	GTTTTAAATC	GGGATGTTT
yukon	TCAAAGACCA	TATTAATATG	GTTCTAAACC	GAGATGTTT
rcn329	TCAAAGATCA	TATTAATATG	GTTTTAAATC	GAGACGTTT
wy28992	TCAAAGACCA	TATTAATATG	GTTTTAAATC	GAGACGTTT
rcn333	TCAAAGACCA	TATTAATATG	GTGCTAAATC	GAGATGTTT
hcn039	TCAAAGACCA	TATTAATATG	GTTCTGAATC	GAGATGTTT
rcn330	TCAAAGATCA	TATCAATATG	GTTTTAAATC	GAGATGTTT
ndr761	TCAAAGACCA	TATCAATATG	GTTTTAAATC	GAGATGTTT
rwa433	TTAAAGATCA	CATTAACATG	GTTTTAAACC	GGGATGTTT
washcc	TTAAAGACCA	CATTAACATG	GTTTTAAACC	GGGATGTTT
washr206	TTAAAGACCA	CATTAACATG	GTTTTAAACC	GGGATGTTT
rwa432	TTAAAGACCA	CATTAACATG	GTTTTAAACC	GGGATGTTT
cnbc2257	TTAAAGATCA	TATAAATATG	GTTTTAAACC	GGGATGTTT
kamloops	TTAAGGATCA	CATAAATATG	GTTTTAAACC	GGGATGTTT
9608868m	TCAAGGACCA	CATCAATATG	GTTCTGAATA	GAGATGTTT
ind	TTAAGGACCA	CATTAATATG	GTTTTGAATC	GAGATGTTT
ndr793	TTAAGGACCA	TATCAACATG	GTCTTGAAACC	GAGATGTTT
wy28923	TTAAGGACCA	CATTAATATG	GTCCTAAACC	GAGATGTTT
ndr805	TTAAGGACCA	TATTAATATG	GTCTTGAAACC	GAGATGTTT
pros	TTAAGGACCA	TATTAATATG	GTCTTGAAACC	GAGATGTTT
rok707	TTAAGGACCA	TATAAATGTA	GTGCTAAATC	GTGATGTGT
mo1234	TTAAGGATCA	CATAAATGTA	GTGTTAAATC	GCGATGTGT
rind4	TCAAAGATCA	TATAAATGTA	GTGTTAAATC	GTGATGTGT
rin378	TTAAGGATCA	TATAAATGTA	GTGTTGAATC	GTGATGTGT
emu26828	TCAAAGACCA	CATTAACCTA	ATTCTCAATA	GAGATTTAT
emu33225	TAAAGGACCA	TGTAATCTA	GTCCTGAATC	GGGATCTAT
emu33260	TAAAGGACCA	TATAAATCTA	GTCCTGCATC	GGGATCTAT
vn757	TTAAAGATCA	TTAAATGTT	GTTGTCACCC	GAGATCTAT

hvimseg	TCAAAGATCA	TATAAATTG	ATTTTAAACC	GAGATGTAT
f16169	TCAAAGATCA	TATAAATTG	ATTTTAAACC	GAGATGTGT
f1478	TCAAAGATCA	TATAAATTG	ATTTTAAACC	GAGATGTAT
f1398	TCAAAGATCA	TATAAATTG	ATTTTAAACC	GAGATGTAT
f16164	TCAAAGATCA	TATAAATTG	ATTTTAAACC	GAGATGTAT
f1210	TCAAAGATCA	TATAAATTG	ATTTTAAACC	GAGATGTAT
f1180	TCAAAGATCA	TATAAATTG	ATTTTAAACC	GAGATGTAT
sc3170	TCAAGGATCA	TATCAATCTA	GTCCTTAATA	GAGACCTCT
rga4950	TTAAGGACCA	TATCAATTG	GTTCTCAATA	GAGATCTAT
rla268	TAAAAGACCA	TATTAACCTG	GTCCTTAACC	GAGATATCT
hviglypre	TAAAAGATCA	TATCAATCTG	GTTCTTAACC	GGGATATT
brazil	CGAGGGATCA	TGTTAACCTT	GTGCTGAATC	GAGATGTAT
b9618005	CACGTGATCA	TGTAACCTC	GTTTTAAATA	GAGATGTAT
andes	CAAGAGACCA	TGTAACCTT	GTCTTAAATA	GAGATGTTT
b9618007	CACGAGATCA	TGTCATCTT	ATTTTAAACA	GGGATGTAT
b9618006	CACGAGATCA	TGTTAATCTC	ATTCTTAACA	GGGATGTAT
pgh9128	CCAGAGACCA	TGTAATCTA	ATTTTAAATA	GAGATGTGT
pgr8480	CCAGAGACCA	TGTAATCTA	ATTTTAAATA	GAGATGTGT
pgr8434	CCAGAGACCA	TGTAATCTA	ATTTTAAATA	GAGATGTGT
pgr8433	CCAGAGACCA	TGTAATCTA	ATTTTAAATA	GAGATGTGT
puumgp	TTCGGGATCA	CATCAAATGTG	ATTGTAAGCC	GTGATTTGT
puugp2m	TTCGGGACCA	TATTAATGTC	ATTGTAGGAC	GTGATCTCT
pvu22418	TGAGAGATCA	TATTAATGTT	ATTGTAGGCC	GTGATCTCT
puuudm	TTAGGGATCA	TATAAATGTA	ATTGTAAGCC	GTGATTTAT
puumseg	TTAGGGACCA	TATAAATGTA	ATTGTGAGTC	GTGATCTAT
puvmvin83	TTAGAGATCA	TATTAATGTG	ATTGTCAGCC	GTGATCTTT
vranicam	TTAGAGATCA	TATTAATGTT	GTGTCAGCC	GTGATCTCT
thai	TACGTGATCA	TATAAATATA	GTTGTTACAA	AGGATATA
hnvdobms	TTAAGGACCA	TCTCAATATA	CTTGTACAA	AAGACATTG
htnhv114	TACGAGACCA	CATTAATATT	CTAGTAACTA	AGGATATTG
htnlee	TGAGGGATCA	TATAAACATC	TTAGTAACAA	AAGACATCG
hanm	TAAGGGACCA	TATAAACATT	TTAGTAACGA	AGGACATTG
seobl	TCCGGGATCA	TATTAATATT	GTTATTTCTA	AAGATATTG
seor11	TTCGGGATCA	TATTAATATT	GTTATTTCTA	AAGATATTG
seo8039	TTCGGGATCA	TATTAATATC	GTTATTTCTA	AAGATATTG
seor22	TTCGGGATCA	TATTAATATC	GTTATTTCTA	AAGATATTG

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